

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:40:49 ; Search time 84 Seconds  
(without alignments)  
225.559 Million cell updates/sec

Title: US-09-674-496D-6

Perfect score: 217  
Sequence: 1 ASNGVCSPEMPGCTGACRCPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	217	100.0	130	1	AL1F_PEA
2	216	99.5	130	1	AL1A_PEA
3	212	97.7	130	1	AL1D_PEA
4	210	96.8	130	1	AL1E_PEA
5	207	95.4	130	1	AL1B_PEA
6	194	89.4	96	2	Q8A1C7
7	173	79.7	130	1	AL1C_PEA
8	159	73.3	98	2	Q8A1B4
9	159	73.3	100	2	Q7XZC3
10	159	73.3	119	1	ALB1_GLYSO
11	156	71.9	140	2	Q7XZC5
12	155	71.4	100	2	Q8A1D7
13	154	71.0	119	1	ALB1_SOYBN
14	153.5	70.7	90	1	ALB1_PHAAN
15	153	70.5	89	1	ALB1_PHAU
16	153	70.5	98	2	Q8A1C9
17	149	68.7	99	2	Q8A1C8
18	148.5	68.4	101	2	Q8A1D1
19	146.5	67.5	101	2	Q8A1D3
20	143.5	66.1	109	2	Q7XZC2
21	138	63.6	99	2	Q8A1D5
22	134	61.8	91	2	Q8A1D6
23	132	60.8	98	2	Q8A1D2
24	130	59.9	142	2	Q7XZC4
25	104.5	48.2	101	2	Q8A1D0
26	100	46.1	59	2	Q8A1C3
27	89	41.0	81	1	ALB1_LUPAN
28	87	40.1	58	2	Q8A1C4
29	86	39.6	58	2	Q8A1B9
30	82	39.2	60	2	Q8A1C1
31	82	37.8	58	2	Q8A1C5

#### ALIGNMENTS

32	73.5	33.9	1642	2	O62055	O62055 caenorhabdi
33	72	33.2	58	2	Q6A1C0	Q6A1C0 vigna subte
34	69	31.8	536	2	Q8I1D9	Q8I1D9 drosophila
35	69	31.8	539	2	Q8M1S4	Q8M1S4 drosophila
36	67	30.9	59	2	Q6A1C6	Q6A1C6 bituminaria
37	65	30.0	1024	2	Q9BX11	Q9BX11 homo sapien
38	65	30.0	1104	1	NFX1_HUMAN	NFX1_HUMAN homo sapien
39	65	30.0	1120	1	Q96EL5	Q96EL5 homo sapien
40	64	29.5	215	2	Q9D7N2	Q9D7N2 mus musculus
41	62.5	28.8	257	2	Q6PQG7	Q6PQG7 phytophthor
42	62.5	28.8	583	1	AXU1_MOUSE	AXU1_MOUSE mus musculus
43	61	28.1	96	2	Q9LJQ3	Q9LJQ3 arabidopsis
44	60	27.6	61	1	MT1A_BOVIN	MT1A_BOVIN bos taurus
45	60	27.6	61	1	MT1A_SHEEP	MT1A_SHEEP ovis aries
46	60	27.6	61	1	MT1B_SHEEP	MT1B_SHEEP ovis aries
47	60	27.6	61	1	MT1C_SHEEP	MT1C_SHEEP ovis aries
48	60	27.6	61	2	Q8M1I4	Q8M1I4 bos taurus
49	60	27.6	61	2	Q6R522	Q6R522 bos mutus g
50	60	27.6	249	2	Q917N9	Q917N9 la piedada-m
51	60	27.6	1785	2	Q8JHV7	Q8JHV7 brachydanio
52	59.5	27.4	79	1	LC81_ARATH	LC81_ARATH arabidopsis
53	59.5	27.4	675	2	Q7QS27	Q7QS27 giardia lam
54	59.5	27.4	685	2	Q7QWD9	Q7QWD9 giardia lam
55	59	27.2	297	2	Q6DH56	Q6DH56 brachydanio
56	59	27.2	420	2	Q6NM65	Q6NM65 brachydanio
57	59	27.2	1799	1	LMB2_MOUSE	LMB2_MOUSE mus musculus
58	59	27.2	1799	2	Q8R0Y0	Q8R0Y0 mus musculus
59	59	27.2	3775	2	Q7PMF9	Q7PMF9 anopheles g
60	58.5	27.0	149	2	Q6PQH2	Q6PQH2 phytophthor
61	58.5	27.0	749	2	Q86TP7	Q86TP7 homo sapien
62	58.5	27.0	804	2	Q7TFP4	Q7TFP4 mus musculus
63	58.5	27.0	818	2	Q8CC59	Q8CC59 mus musculus
64	58.5	27.0	818	2	Q9DBC8	Q9DBC8 mus musculus
65	58.5	27.0	1035	2	Q7QR01	Q7QR01 giardia lam
66	58.5	27.0	1114	2	Q9JKW7	Q9JKW7 mus musculus
67	58.5	27.0	1761	2	Q86XN2	Q86XN2 homo sapien
68	58	26.7	60	2	Q6A1C2	Q6A1C2 mundulea se
69	58	26.7	285	2	Q7VBZ4	Q7VBZ4 prochloroco
70	58	26.7	418	2	Q8LNM4	Q8LNM4 oryza sativ
71	58	26.7	1801	1	LMB2_RAT	LMB2_RAT rattus norv
72	58	26.7	23015	2	Q8I0I8	Q8I0I8 drosophila
73	57	26.3	174	1	CYS3_OSTOS	CYS3_OSTOS ostertagia
74	57	26.3	194	2	Q9N9C6	Q9N9C6 ostertagia
75	57	26.3	291	2	Q8MKQ8	Q8MKQ8 drosophila
76	56.5	26.0	271	1	K105_HUMAN	K105_HUMAN homo sapien
77	56.5	26.0	277	2	Q6V4H5	Q6V4H5 procambatus
78	56.5	26.0	1156	2	Q963T3	Q963T3 aedes aegyp
79	56	25.8	56	1	M87F_DROME	M87F_DROME drosophila
80	56	25.8	61	1	MT1_BOVIN	MT1_BOVIN bos taurus
81	56	25.8	194	2	Q7PI78	Q7PI78 anopheles g
82	56	25.8	264	2	Q66T09	Q66T09 brachydanio
83	56	25.8	270	1	DAPF_RICPR	DAPF_RICPR rickettsia
84	56	25.8	274	2	Q6W4T8	Q6W4T8 brachydanio
85	56	25.8	302	2	Q96H92	Q96H92 homo sapien
86	56	25.8	358	2	Q8K2C1	Q8K2C1 mus musculus
87	56	25.8	375	2	Q20002	Q20002 caenorhabdi
88	56	25.8	388	2	Q6PJL7	Q6PJL7 homo sapien
89	56	25.8	405	2	Q8S260	Q8S260 drosophila
90	56	25.8	426	2	Q67U09	Q67U09 oryza sativ
91	56	25.8	429	2	Q8MUJ9	Q8MUJ9 homo sapien
92	56	25.8	435	2	Q7YR70	Q7YR70 canis famli
93	56	25.8	452	1	AAMP_HUMAN	AAMP_HUMAN homo sapien
94	56	25.8	525	2	Q6X1X4	Q6X1X4 feldmannia
95	56	25.8	609	2	Q7QNX8	Q7QNX8 giardia lam
96	56	25.8	813	1	YTOJ_CAEEL	YTOJ_CAEEL caenorhabdi
97	55.5	25.6	131	2	Q86K22	Q86K22 dictyosteli
98	55.5	25.6	747	2	Q8VHF4	Q8VHF4 mus musculus
99	55.5	25.6	1004	2	Q8CGA7	Q8CGA7 mus musculus
100	55.5	25.6	1034	2	Q8VHL7	Q8VHL7 mus musculus

```
RESULT 1
AL1F_PEA
ID AL1F_PEA STANDARD; PRT; 130 AA.
AC P62931; P08687; Q40999; Q7X9N3; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 F precursor (PAL F) (PaaAlb005/PaaAlb011) [Contains: Albumin
DE 1 F chain b (PALb F) (Leginsulin F); Albumin 1 F chain a (PALa F)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Frisson; TISSUE=Seed;
RA Louis S., Delobel B., Gressent F., Rahloui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
RN [2]
RP SEQUENCE OF 27-63, AND FUNCTION.
RA Delobel B., Grenier A., Gueguen J., Ferrasson E., Mbailao M.;
RT "Use of a polypeptide derived from a PALb legume albumen as
RT insecticide.";
RL Patent number WO9958695, 07-MAY-1999.
RN [3]
RP STRUCTURE BY NMR OF 27-63, AND DISULFIDE BONDS.
RX PubMed=14556622; DOI=10.1021/bi0348031;
RA Jouvansal L., Quillien L., Ferrasson E., Rahbe Y., Gueguen J.,
RA Vovelle F.;
RT "PALb, an insecticidal protein extracted from pea seeds (Pisum
RT sativum): 1H-2-D NMR study and molecular modelling.";
RL Biochemistry 42:11915-11923(2003).
RN [4]
RP FUNCTION.
RX PubMed=12755698;
RA Gressent F., Rahloui I., Rahbe Y.;
RT "Characterization of a high-affinity binding site for the pea albumin
RT 1b endomotoxin in the weevil Sitophilus.";
RL Eur. J. Biochem. 270:2429-2435(2003).
CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide (By similarity). Toxic to various insects through binding
CC to a high affinity binding site in the insect gut.
CC -1- PTM: The C-terminal glycine may be removed from PALb.
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; AJ574793; CAS00465.1; -
DR PDB; 1P8B; NMR; A=27-63.
DR InterPro; IPR011036; PH related.
KW 3D-structure; Direct protein sequencing; Plant toxin;
KW Seed storage protein; Signal.
FT SIGNAL 1 26 Albumin 1 F chain b.
FT CHAIN 27 63 Potential.
FT PROPEP 64 69 Potential.
FT CHAIN 70 122 Albumin 1 F chain a.
FT PROPEP 123 130 Potential.
FT DISULFID 29 46 By similarity.
FT DISULFID 33 48 By similarity.
FT DISULFID 41 58 By similarity.
SQ SEQUENCE 130 AA; 13912 MW; 1371D80F333E0EFF CRC64;
Query Match 99.5%; Score 216; DB 1; Length 130;
Best Local Similarity 97.3%; Pred. No. 2e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
AL1A_PEA
ID AL1A_PEA STANDARD; PRT; 130 AA.
AC P62926; P08687; Q40999; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 A precursor (PAL A) [Contains: Albumin 1 A chain b (PALb A)
DE (Leginsulin A); Albumin 1 A chain a (PALa A)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Greenfeast; TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kott A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide. Toxic to various insects through binding to a high
CC affinity binding site in the insect gut (By similarity).
CC -1- TISSUE SPECIFICITY: Major component of both the cotyledons and
CC embryonic axes of mature seeds.
CC -1- DEVELOPMENTAL STAGE: Increasing expression during seed development
CC followed by a rapid degradation during the first days of seed
CC germination.
CC -1- PTM: The C-terminal glycine may be removed from PALb.
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; M13709; AAA33638.1; -
DR PIR; A25014; A25014.
DR InterPro; IPR011036; PH related.
KW Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 63 Albumin 1 A chain b.
FT PROPEP 64 69 Potential.
FT CHAIN 70 122 Albumin 1 A chain a.
FT PROPEP 123 130 Potential.
FT DISULFID 29 46 By similarity.
FT DISULFID 33 48 By similarity.
FT DISULFID 41 58 By similarity.
SQ SEQUENCE 130 AA; 13912 MW; 1371D80F333E0EFF CRC64;
Query Match 99.5%; Score 216; DB 1; Length 130;
Best Local Similarity 97.3%; Pred. No. 2e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 130 AA; 13913 MW; FD58E2D3C99D1644 CRC64;
Query Match 100.0%; Score 217; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCNGVCSPPMPCCGTSACRCIPVGLVIGYCRNPSSG 37
DB 27 ASCNGVCSPPMPCCGTSACRCIPVGLVIGYCRNPSSG 63

RESULT 2
AL1A_PEA
ID AL1A_PEA STANDARD; PRT; 130 AA.
AC P62926; P08687; Q40999; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 A precursor (PAL A) [Contains: Albumin 1 A chain b (PALb A)
DE (Leginsulin A); Albumin 1 A chain a (PALa A)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Greenfeast; TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kott A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide. Toxic to various insects through binding to a high
CC affinity binding site in the insect gut (By similarity).
CC -1- TISSUE SPECIFICITY: Major component of both the cotyledons and
CC embryonic axes of mature seeds.
CC -1- DEVELOPMENTAL STAGE: Increasing expression during seed development
CC followed by a rapid degradation during the first days of seed
CC germination.
CC -1- PTM: The C-terminal glycine may be removed from PALb.
CC -----
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CC -----
DR EMBL; M13709; AAA33638.1; -
DR PIR; A25014; A25014.
DR InterPro; IPR011036; PH related.
KW Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 63 Albumin 1 A chain b.
FT PROPEP 64 69 Potential.
FT CHAIN 70 122 Albumin 1 A chain a.
FT PROPEP 123 130 Potential.
FT DISULFID 29 46 By similarity.
FT DISULFID 33 48 By similarity.
FT DISULFID 41 58 By similarity.
SQ SEQUENCE 130 AA; 13912 MW; 1371D80F333E0EFF CRC64;
Query Match 99.5%; Score 216; DB 1; Length 130;
Best Local Similarity 97.3%; Pred. No. 2e-17;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCNGVCSPPMPCCGTSACRCIPVGLVIGYCRNPSSG 37
```

[illegible]

27 ASCNGVCSPPFPPCGSSACRCIPVGLVGVCRHPSG 63

RESULT 5  
AL1B\_PEA  
ID -AL1B\_PEA STANDARD; Q40999; Q9M3X4; PRT; 130 AA.  
AC P62927; P08687; Q40999; Q9M3X4;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Albumin 1 B precursor (PA1 B) [Contains: Albumin 1 B chain b (PA1B B)  
DE (Leguminsulin B); Albumin 1 B chain a (PA1A B)].  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.  
RC STRAIN=cv. Greenfeast; TISSUE=Seed;  
RX MEDLINE=86278210; PubMed=3755437;  
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
RT "Gene structure, protein structure, and regulation of the synthesis of  
RT a sulfur-rich protein in pea seeds.";  
RL J. Biol. Chem. 261:11124-11130(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Birte; TISSUE=Cotyledon;  
RX Domoney C., Ellis N., Wellham T.;  
RA "Genetic loci controlling albumin synthesis in Pisum.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: PA1B binds to basic 7S globulin (BG) and stimulates its  
CC phosphorylation activity. Involved in the signal transduction  
CC system to regulate the growth and differentiation as a hormone  
CC peptide. Toxic to various insects through binding to a high  
CC affinity binding site in the insect gut (by similarity).  
CC -!- TISSUE SPECIFICITY: Major component of both the cotyledons and  
CC embryonic axes of mature seeds.  
CC -!- DEVELOPMENTAL STAGE: Increasing expression during seed development  
CC followed by a rapid degradation during the first days of seed  
CC germination.  
CC -!- PTM: The C-terminal glycine may be removed from PA1B.  
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CC  
CC EMBL; M13790; AA33639.1; -.  
DR EMBL; AJ276882; CAB82859.1; -.  
DR InterPro; IPR011036; PH-related.  
KW Plant toxin; Seed storage protein; Signal.  
FT SIGNAL 1 26 Potential.  
FT CHAIN 27 63 Albumin 1 B chain b.  
FT PROPEP 64 69 Potential.  
FT CHAIN 70 122 Albumin 1 B chain a.  
FT PROPEP 123 130 Potential.  
FT DISULFID 29 46 By similarity.  
FT DISULFID 33 48 By similarity.  
FT DISULFID 41 58 By similarity.  
FT CONFLICT 10 10 M -> I (in Ref. 2).  
FT CONFLICT 120 120 Q -> P (in Ref. 2).  
SQ SEQUENCE 130 AA; 13970 MW; F8B134A33490F5F CRC64;  
Query Match 95.4%; Score 207; DB 1; Length 130;  
Best Local Similarity 91.9%; Pred. No. 2.2e-16;  
Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ASCNGVCSPPFPPCGSSACRCIPVGLVGVCRHPSG 37  
|||||

RESULT 6  
Q6A1C7  
ID Q6A1C7 PRELIMINARY; PRT; 96 AA.  
AC Q6A1C7;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Putative albumin 1 precursor (Fragment).  
GN Name=pa1;  
OS Vicia hirsuta.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
OX NCBI\_TaxID=3910;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
RT "Gene structure, protein structure, and regulation of the synthesis of  
RT a sulfur-rich protein in pea seeds.";  
RL J. Biol. Chem. 261:11124-11130(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Louis S., Delobel B., Gressent F., Rahioui I., Dupont G., Diol O.,  
RA Chessel D., Rahbe Y.;  
RT "Broad screening of the legume family for variability of insecticidal  
RT activities and occurrence of seed albumin 1b toxins.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784951; CAH05251.1; -.  
KW SIGNAL 1 26 Potential.  
FT CHAIN 27 63 putative albumin 1b.  
FT CHAIN 69 >96 putative albumin 1a.  
FT NON\_TER 96 96  
SQ SEQUENCE 96 AA; 10546 MW; DD8EF1B021A73DD7 CRC64;  
Query Match 89.4%; Score 194; DB 2; Length 96;  
Best Local Similarity 86.5%; Pred. No. 5.4e-15;  
Matches 32; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ASCNGVCSPPFPPCGSSACRCIPVGLVGVCRHPSG 37  
|||||  
Db 27 AECNGVCSPPFPPCGSSACRCIPVGLVGVCRHPSG 63  
|||||  
RESULT 7  
AL1C\_PEA  
ID -AL1C\_PEA STANDARD; PRT; 130 AA.  
AC P62928; P08687; Q40999; Q7XZC0; Q9M3X4;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Albumin 1 C precursor (PA1 C) [Contains: Albumin 1 C chain  
DE b (PA1B C) (Leguminsulin C); Albumin 1 C chain a (PA1A C)].  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Frisson; TISSUE=Seed;  
RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,  
RA Vallier A., Rahbe Y.;  
RT "Molecular and biological screening for insect-toxic seed albumins  
RT from four legume species.";  
RL Plant Sci. 167:705-714(2004).  
RN [2]  
RP SEQUENCE OF 27-63, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.  
RC TISSUE=Seed;





[illegible]

```

RESULT 13
ALBI SOYBN STANDARD; PRT; 119 AA.
ID ALBI SOYBN STANDARD; PRT; 119 AA.
AC Q39837; O49854;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Albumin 1 precursor (Al) [Chain: Albumin 1 chain b (Alb)
DE (Leginulin); Albumin 1 chain a (Ala)].
DE Leginulin; Albumin 1 chain a (Ala)].
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids;
OC Eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC NCBI_TaxId:3847;
OX NCBI_TaxId:3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagishirome; TISSUE=Radicle;
RX MEDLINE=94357216; PubMed=8076638;
RA Watanabe Y., Barbashov S.F., Komatsu S., Miyagi M.,
RA Tsunawasa S., Hirano H.;

```



RT "A possible physiological function and the tertiary structure of a 4-  
RL kDa peptide in legumes.";  
CC Eur. J. Biochem. 270:1269-1276(2003).  
CC -1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its  
CC phosphorylation activity (By similarity).  
CC -1- PFM: The C-terminal glycine may be removed from Alb.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; AB052881; BAB1938.1; --  
DR HSP3; Q39837; LU08.  
KW Plant toxin; Seed storage protein; Signal.  
FT SIGNAL 1 1 Potential.  
FT CHAIN <1 1 Albumin 1 chain b (By similarity).  
FT PROPEP 39 38 Potential.  
FT CHAIN 47 >89 Albumin 1 chain a (Potential).  
FT DISULFID 4 21 By similarity.  
FT DISULFID 8 23 By similarity.  
FT DISULFID 16 33 By similarity.  
FT NON TER 89 89  
SQ SEQUENCE 89 AA; 9711 MW; 4ADEB9797083135B CRC64;

Query Match 70.5%; Score 153; DB 1; Length 89;  
Best Local Similarity 64.9%; Pred. No. 2.9e-10;  
Matches 24; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37  
DB 2 ADNGAGCSPPFMPGCGTSACRCIPVGLVIGYCRNP 38

## RESULT 16

ID Q6A1C9 PRELIMINARY; PRT; 98 AA.  
AC Q6A1C9; (Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Putative albumin 1 precursor (Fragment).  
GN Name-pal;  
OS Onobrychis viciifolia (Common sainfoin).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Hedyosarea; Onobrychis.  
OX NCBI\_TaxID=3882;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
RT "Gene structure, protein structure, and regulation of the synthesis of  
RT a sulfur-rich protein in pea seeds.";  
RL J. Biol. Chem. 261:11124-11130(1986).  
RN [2]

RP SEQUENCE FROM N.A.  
RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,  
RA Chessel D., Rabhe Y.;  
RT "Broad screening of the legume family for variability of insecticidal  
RT activities and occurrence of seed albumin lb toxins.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784949; CAH05249.1; --  
KW Signal.  
FT SIGNAL 1 28 Potential.  
FT CHAIN 29 63 putative albumin 1b.  
FT CHAIN 71 >98 putative albumin 1a.  
FT NON TER 98 98  
SQ SEQUENCE 98 AA; 10830 MW; 03072C77178A1E83 CRC64;

Query Match 70.5%; Score 153; DB 2; Length 98;  
Best Local Similarity 65.7%; Pred. No. 3.1e-10;  
Matches 23; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 SCNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNPS 36  
DB 28 ACDGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 62

## RESULT 17

Q6A1C8 PRELIMINARY; PRT; 99 AA.  
AC Q6A1C8; (Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Putative albumin 1 precursor (Fragment).  
GN Name-pal;  
OS Trigonella foenum-graecum (Fenugreek).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trigonella.  
OX NCBI\_TaxID=78534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
RT "Gene structure, protein structure, and regulation of the synthesis of  
RT a sulfur-rich protein in pea seeds.";  
RL J. Biol. Chem. 261:11124-11130(1986).  
RN [2]

RP SEQUENCE FROM N.A.  
RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,  
RA Chessel D., Rabhe Y.;  
RT "Broad screening of the legume family for variability of insecticidal  
RT activities and occurrence of seed albumin lb toxins.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784950; CAH05250.1; --  
KW Signal.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 64 putative albumin 1b.  
FT CHAIN 72 >99 putative albumin 1a.  
FT NON TER 99 99  
SQ SEQUENCE 99 AA; 10783 MW; 94D20EAD462018B4 CRC64;

Query Match 68.7%; Score 149; DB 2; Length 99;  
Best Local Similarity 72.7%; Pred. No. 9e-10;  
Matches 24; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 CNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 35  
DB 30 CSGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 62

## RESULT 18

Q6A1D1 PRELIMINARY; PRT; 101 AA.  
AC Q6A1D1; (Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Putative albumin 1 precursor (Fragment).  
GN Name-pal;  
OS Mundulea sericea.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Millettiae; Mundulea.  
OX NCBI\_TaxID=54460;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;

RT "Gene structure, protein structure, and regulation of the synthesis of  
 RL a sulfur-rich protein in pea seeds.";  
 J. Biol. Chem. 261:11124-11130(1986).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,  
 RA Chessel D., Rahbe Y.;  
 RT "Broad screening of the legume family for variability of insecticidal  
 RT activities and occurrence of seed albumin lb toxins.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ784947; CAH05247.1; --  
 KW Signal.  
 FT SIGNAL. 1 24 Potential.  
 FT CHAIN 25 64 putative albumin lb.  
 FT CHAIN 71 >101 putative albumin la.  
 FT NON TER 101 101  
 SQ SEQUENCE 101 AA; 11068 MW; 26ECD6B970BD10E2 CRC64;  
 Query Match 68.4%; Score 148.5; DB 2; Length 101;  
 Best Local Similarity 74.4%; Pred. No. 1e-09;  
 Matches 29; Conservative 2; Mismatches 5; Indels 3; Gaps 2;  
 Qy 2 SCNG--VCSFPEPPCGTSA-CRCIPVGLVIGYCRNPSSG 37  
 Db 26 SCNGRDWCSPFPEPPCGDAQNCRCIPVGLVIGYCRHPSSG 64  
 RESULT 19  
 Q6A1D3 PRELIMINARY; PRT; 101 AA.  
 ID Q6A1D3  
 AC Q6A1D3;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE Putative albumin 1 precursor (Fragment).  
 GN Name=pa1;  
 OS Lonchocarpus capassa (Apple-leaf).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Millettieae;  
 OC Lonchocarpus.  
 OK NCBI\_TaxID=3926;  
 RN SEQUENCE FROM N.A.  
 RP Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
 RT "Gene structure, protein structure, and regulation of the synthesis of  
 RT a sulfur-rich protein in pea seeds.";  
 RL J. Biol. Chem. 261:11124-11130(1986).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,  
 RA Chessel D., Rahbe Y.;  
 RT "Broad screening of the legume family for variability of insecticidal  
 RT activities and occurrence of seed albumin lb toxins.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ784945; CAH05245.1; --  
 KW Signal.  
 FT SIGNAL. 1 25 Potential.  
 FT CHAIN 26 65 putative albumin lb.  
 FT CHAIN 74 >101 putative albumin la.  
 FT NON TER 101 101  
 SQ SEQUENCE 101 AA; 11003 MW; 0B8A138465E7C19B CRC64;  
 Query Match 67.5%; Score 146.5; DB 2; Length 101;  
 Best Local Similarity 70.0%; Pred. No. 1.8e-09;  
 Matches 28; Conservative 3; Mismatches 6; Indels 3; Gaps 2;  
 Qy 1 ASCNG--VCSFPEPPCGTSA-CRCIPVGLVIGYCRNPSSG 37  
 Db 26 ASCNGRDWCSPFPEPPCGDATTNCRCPWGLVVGQCVHPSSG 65

RESULT 20  
 Q7XZC2 PRELIMINARY; PRT; 109 AA.  
 ID Q7XZC2  
 AC Q7XZC2;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DE Albumin 1 precursor (Fragment).  
 GN Name=pa1;  
 OS Phaseolus vulgaris (Kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 OK NCBI\_TaxID=3885;  
 RN SEQUENCE FROM N.A.  
 RP Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,  
 RA Vallier A., Rahbe Y.;  
 RT "Molecular and biological screening for insect-toxic seed albumins  
 RT from four legume species.";  
 RL Plant Sci. 167:705-714(2004).  
 DR EMBL; AJ574792; CAE00464.1; --  
 DR HSP; Q39837; LU08.  
 KW Signal.  
 FT SIGNAL. 1 27 Potential.  
 FT CHAIN 28 65 Alb, albumin lb.  
 FT CHAIN 74 >109 Ala, albumin la.  
 FT NON TER 109 109  
 SQ SEQUENCE 109 AA; 11923 MW; E420417E90D351AE CRC64;  
 Query Match 66.1%; Score 143.5; DB 2; Length 109;  
 Best Local Similarity 72.2%; Pred. No. 4.2e-09;  
 Matches 26; Conservative 1; Mismatches 8; Indels 1; Gaps 1;  
 Qy 3 CNGVCSPFPEPPCG-TSACRCIPVGLVIGYCRNPSSG 37  
 Db 30 CSGVCSPFPEPPCGSTRDCRCIPYGLFAGACTYPSG 65  
 RESULT 21  
 Q6A1D5 PRELIMINARY; PRT; 99 AA.  
 ID Q6A1D5  
 AC Q6A1D5;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE Putative albumin 1 precursor (Fragment).  
 GN Name=pa1;  
 OS Bituminaria bituminosa.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Psoraleae;  
 OC Bituminaria.  
 OK NCBI\_TaxID=53836;  
 RN SEQUENCE FROM N.A.  
 RP Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
 RT "Gene structure, protein structure, and regulation of the synthesis of  
 RT a sulfur-rich protein in pea seeds.";  
 RL J. Biol. Chem. 261:11124-11130(1986).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,  
 RA Chessel D., Rahbe Y.;  
 RT "Broad screening of the legume family for variability of insecticidal  
 RT activities and occurrence of seed albumin lb toxins.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ784943; CAH05243.1; --  
 KW Signal.  
 FT SIGNAL. 1 27 Potential.  
 FT CHAIN 28 62 putative albumin lb.  
 FT CHAIN 72 >99 putative albumin la.



Search completed: March 28, 2005, 09:00:06  
Job time : 87 secs

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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:50:15 ; Search time 23.5 Seconds  
(without alignments)  
151.490 Million cell updates/sec

Title: us-09-674-496d-6

Perfect score: 217

Sequence: 1 ASCNGVCSPEMPPGTSACRCIPVLGLVGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	99.5	130	2 A25014	albumin precursor
2	154	71.0	119	2 S48192	insulin-like growth
3	73.5	33.9	1642	2 T19130	hypothetical prote
4	65	30.0	1104	2 T38869	transcription fact
5	62	28.6	1797	2 A55677	laminin beta-2 cha
6	60	27.6	61	1 SMBO2	metallothionein II
7	60	27.6	61	2 S00810	metallothionein Ia
8	60	27.6	61	2 S00809	metallothionein Ib
9	60	27.6	1801	1 MWRYS	laminin beta-2 cha
10	58	26.7	174	2 B48454	cathepsin B-like c
11	57	26.3	174	2 B48454	cathepsin B-like c
12	56	25.8	56	1 WTFE	testis-specific pr
13	56	25.8	61	2 A23889	metallothionein I
14	56	25.8	270	2 F71699	diaminopimelate ep
15	56	25.8	375	2 T16248	hypothetical prote
16	56	25.8	452	2 T39383	angio-associated m
17	56	25.8	813	2 T21192	hypothetical prote
18	55	25.3	61	2 T48173	metallothionein II
19	55	25.3	1798	2 S53869	laminin beta-2 cha
20	55	25.3	2437	2 S42612	transmembrane prot
21	55	25.3	3075	2 S14458	laminin alpha-1 ch
22	54.5	25.1	1574	2 T13954	MEGF6 protein - ra
23	53.5	24.7	85	2 T05719	metallothionein II
24	53.5	24.7	87	2 F88369	small cysteine-ric
25	53.5	24.7	1160	2 F88369	protein unc-52 [im
26	53.5	24.7	2295	2 C88369	protein unc-52 [im
27	53.5	24.7	3375	2 T19821	hypothetical prote
28	53	24.4	61	1 SMMS2	metallothionein II
29	53	24.4	61	2 T57572	metallothionein II

30	53	24.4	450	2	T17234	hypothetical prote
31	52	24.0	61	1	SMHY2C	metallothionein II
32	52	24.0	61	2	S18403	metallothionein II
33	52	24.0	61	2	T48116	metallothionein II
34	52	24.0	74	2	S25773	testis-specific pr
35	52	24.0	274	2	F64090	diaminopimelate ep
36	52	24.0	336	2	S33879	plasma precursor
37	52	24.0	408	1	QRHUBE	beta-3-adrenergic
38	52	24.0	414	1	QRHUB3	beta-3-adrenergic
39	51.5	23.7	861	2	B49847	nitrate reductase
40	51.5	23.7	1786	1	MMHUB1	laminin beta-1 cha
41	51.5	23.7	4544	1	S02392	alpha-2-macroglobu
42	51.5	23.7	4545	1	S25111	alpha-2-macroglobu
43	51.5	23.7	6420	2	T30283	polyketide synthase
44	51	23.5	61	1	SMRT2	metallothionein II
45	51	23.5	151	2	S60314	hair keratin cyste
46	51	23.5	281	1	ZBBE12	30.2K zinc-binding
47	51	23.5	322	2	T27966	hypothetical prote
48	51	23.5	457	2	T46332	hypothetical prote
49	51	23.5	473	2	A56175	adhesive plaque pr
50	51	23.5	706	2	A48084	env polypeptide kin
51	51	23.5	856	1	A44963	hypothetical prote
52	51	23.5	1131	2	T38744	MEGF2 protein - hu
53	51	23.5	1364	2	T00250	laminin alpha-1 ch
54	51	23.5	3084	1	MMMSA	hypothetical prote
55	50.5	23.3	160	2	T25185	hypothetical prote
56	50.5	23.3	290	2	T21185	hypothetical prote
57	50.5	23.3	309	2	T28708	hypothetical prote
58	50.5	23.3	379	2	A59180	Wnt inhibitory fac
59	50.5	23.3	1101	2	T16840	hypothetical prote
60	50.5	23.3	1888	2	D86236	protein F14N23.5 l
61	50.5	23.3	1808	2	T15099	hypothetical prote
62	50	23.0	61	1	SMHUIG	metallothionein I
63	50	23.0	61	1	SMHY1C	metallothionein I
64	50	23.0	270	2	C97772	diaminopimelate ep
65	50	23.0	316	2	T33776	hypothetical prote
66	50	23.0	342	2	A48454	cathepsin B-like c
67	50	23.0	579	2	JC7629	membrane-type friz
68	50	23.0	915	1	A55144	autocatalin precu
69	49.5	22.8	160	2	S28290	hypothetical prote
70	49.5	22.8	228	2	S45677	proteinase inhibit
71	49.5	22.8	245	1	A47539	homeotic protein g
72	49.5	22.8	372	2	T29359	hypothetical prote
73	49.5	22.8	400	2	S32804	beta-3-adrenergic
74	49.5	22.8	480	2	AF3057	glycogen synthase
75	49.5	22.8	480	2	H98228	p-selectin precurs
76	49.5	22.8	768	2	A42755	hypothetical prote
77	49.5	22.8	787	2	PN0677	hypothetical prote
78	49.5	22.8	1006	2	JC5526	kinase-defective E
79	49	22.6	55	2	S25774	testis-specific pr
80	49	22.6	61	1	SMHUIE	metallothionein I
81	49	22.6	61	1	SMHUIF	metallothionein I
82	49	22.6	61	1	SMHUI2	metallothionein 2
83	49	22.6	61	1	SMHUI1	metallothionein 1
84	49	22.6	61	1	SMHUI2	metallothionein 2
85	49	22.6	61	1	SMHUI1	metallothionein 1
86	49	22.6	61	1	SMRT1	metallothionein I
87	49	22.6	61	1	S4574	metallothionein-1
88	49	22.6	61	2	S47652	metallothionein 1X
89	49	22.6	61	2	B23889	metallothionein 2
90	49	22.6	61	2	S00811	metallothionein 1
91	49	22.6	108	2	S43154	diaminopimelate ep
92	49	22.6	145	2	T15608	hypothetical prote
93	49	22.6	214	2	S15326	fimbrial protein M
94	49	22.6	214	2	T32177	hypothetical prote
95	49	22.6	276	2	G82986	diaminopimelate ep
96	49	22.6	277	2	I52825	gene MAC25 protein
97	49	22.6	282	2	S50031	proscacyclin-stimu
98	49	22.6	334	2	A48151	sperm tail protein
99	49	22.6	335	2	T31730	hypothetical prote
100	49	22.6	348	2	B48435	cysteine proteinase

ALIGNMENTS

RESULT 1

A25014  
albumin precursor - garden pea  
C;Species: Pisum sativum (garden pea)  
C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 09-Jul-2004  
C;Accession: A25014  
R;Higgins, T.J.V.; Chandler, P.M.; Randall, P.J.; Spencer, D.; Beach, L.R.; Blagrove, R.  
J. Biol. Chem. 261, 11124-11130, 1986  
A;Title: Gene structure, protein structure, and regulation of the synthesis of a sulfur-  
A;Reference number: A25014; MUID:86278210; PMID:3755437  
A;Accession: A25014  
A;Molecule type: DNA  
A;Residues: 1-130 <HIG>  
A;Cross-references: UNIPROT:P08687; GB:M13709; NID:g169024; PIDN:AAA33638.1; PID:g169025  
C;Genetics:  
A;Introns: 17/1  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-130/Product: albumin #status predicted <MAT>

Query Match 99.5%; Score 216; DB 2; Length 130;  
Best Local Similarity 97.3%; Pred. No. 1.6e-17;  
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37  
|||||  
Db 27 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 63  
|||||

RESULT 2

S48192  
insulin-like growth factor S11 precursor - soybean  
N;Alternate names: leguminin  
C;Species: Glycine max (soybean)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S48192  
R;Watanabe, Y.; Barbashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunasawa, S.;  
Eur. J. Biochem. 224, 167-172, 1994  
A;Title: A peptide that stimulates phosphorylation of the plant insulin-binding protein.  
A;Reference number: S48192; MUID:94357216; PMID:8076638  
A;Accession: S48192  
A;Molecule type: mRNA; protein  
A;Residues: 1-119 <MAT>  
A;Cross-references: UNIPROT:Q39837; GB:D17396; NID:g498167; PIDN:BAA04219.1; PID:g498168  
R;Barbashov, S.F.; Egorov, T.A.  
Mol. Biol. (Mosk.) 24, 953-961, 1990  
A;Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cell g  
A;Reference number: PN0115; MUID:91066897; PMID:2250683  
A;Accession: PN0116

A;Molecule type: protein  
A;Residues: 20-30; M, 32-39 <BAR>  
F;1-19/Domain: propeptide #status predicted <PRO>  
F;20-56/Product: insulin-like growth factor S11 #status experimental <MAT>

Query Match 71.0%; Score 154; DB 2; Length 119;  
Best Local Similarity 59.5%; Pred. No. 1.4e-10;  
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37  
|||||  
Db 20 ADCNGACSPFVPPCRSDRCRCPVIGLVFGCIHPTG 56  
|||||

RESULT 3

T19130  
hypothetical protein C09F9.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19130  
R;Smey, R.  
submitted to the EMBL Data Library, November 1996

A;Reference number: Z19078

A;Accession: T19130  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1642 <WIL>  
A;Cross-references: UNIPROT:O62055; EMBL:Z81465; PIDN:CAB03861.1; GSPDB:GN000020; CESP:CO;  
A;Experimental source: clone C09F9  
C;Genetics:  
A;Gene: CESP:C09F9.2  
A;Map position: 2  
A;Introns: 75/3; 103/2; 220/1; 552/1; 1500/3; 1517/1; 1578/3

Query Match 33.9%; Score 73.5; DB 2; Length 1642;  
Best Local Similarity 37.8%; Pred. No. 1.12;  
Matches 14; Conservative 5; Mismatches 13; Indels 5; Gaps 1;

QY 1 ASNGVCSPPFMPGCGTSACRCIPVGLVIGYCRNP 37  
|||||  
Db 509 ADCFSIFTRSECTDCGSAACACLIQ-----GYARNPQG 540  
|||||

RESULT 4

I38869  
transcription factor NFX1 [imported] - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I38869  
R;Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.  
J. Exp. Med. 180, 1763-1774, 1994  
A;Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the  
n and functions as a transcriptional repressor.  
A;Reference number: I38869; MUID:95053707; PMID:7964459  
A;Accession: I38869

A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1104 <RES>  
A;Cross-references: UNIPROT:Q12986; EMBL:U15306; NID:g563216; PIDN:AAA69517.1; PID:g56321;  
F;338-398/Domain: RING finger homology <RRN>

Query Match 30.0%; Score 65; DB 2; Length 1104;  
Best Local Similarity 34.1%; Pred. No. 8;  
Matches 15; Conservative 4; Mismatches 15; Indels 10; Gaps 3;

QY 2 SCNGVCSPPFMPGCG---TSACRC-----IPVGLVIG-YCRNP 35  
|||||  
Db 440 SCNLLCHPGCPCPAFMTKTCGGRTRTVRCGQAVSVHCNP 483  
|||||

RESULT 5

A55677  
laminin beta-2 chain precursor (version 1) - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 17-Mar-1999  
C;Accession: A55677  
R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliand, M.F.;  
Genomics 24, 243-252, 1994  
A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca  
A;Reference number: A55677; MUID:95213013; PMID:7698745

A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1797 <WEW>  
A;Cross-references: GB:X79683  
C;Genetics:  
A;Gene: GDB:LAMB2

A;Cross-references: GDB:132363; OMIM:150325  
A;Map position: 3p21.3-3p21.2  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1797/Product: laminin beta-2 chain #status predicted <MAT>  
F;283-344/Domain: laminin-type EGF-like homology <LE01>  
F;347-407/Domain: laminin-type EGF-like homology <LE02>

Eur. J. Biochem. 160, 579-585, 1986  
A;Title: Structure and regulation of the sheep metallothionein-Ia gene.  
A;Reference number: I46414; MUID:87053978; PMID:3780723  
A;Accession: I46414  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A;Residues: 1-49, S', 51-61 <PET2>  
A;Cross-references: EMBL:X04626; NID:g4218467  
R;Peterson, M.G.; Laddins, I.; Danks, D.M.; Mercer, J.F.  
Eur. J. Biochem. 143, 507-511, 1984  
A;Title: Cloning and sequencing of a sheep metallothionein cDNA.  
A;Reference number: I46559; MUID:85003624; PMID:6434305  
A;Accession: I46559  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A;Residues: 1-61 <PET3>  
A;Cross-references: EMBL:X00953; NID:g1825; PIDN:CAA25464.1; PID:g1826  
C;Genetics:  
A;Introns: 10/1; 32/1  
C;Superfamily: metallothionein

Query Match            27.6%;    Score 60; DB 2; Length 61;  
Best Local Similarity 44.4%; Pred.No.3.3;  
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

Qy         2 SCNG--VCSPFEMPFGCTGTCACRCIPVG 26  
            |||                                |||  
Db         14 SCAGSCTCKACRCPSCKKSCGCCCPVG 40

RESULT 8  
S00810  
metallothionein Ic - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: S00810  
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.  
Eur. J. Biochem. 174, 417-424, 1988  
A;Title: The sheep metallothionein gene family. Structure, sequence and evolutionary re  
A;Reference number: S00808; MUID:88254812; PMID:3383853  
A;Accession: S00810  
A:Molecule type: DNA  
A;Residues: 1-61 <PET>  
A;Cross-references: UNIPROT:P09578; EMBL:X07974; NID:gl340; PIDN:CAA30786.1; PID:gi341  
C;Genetics:  
A;Introns: 10/1; 32/1  
C;Superfamily: metallothionein

Query Match            27.6%;    Score 60; DB 2; Length 61;  
Best Local Similarity 44.4%; Pred.No.3.3;  
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

Qy         2 SCNG--VCSPFEMPFGCTGTCACRCIPVG 26  
            |||                                |||  
Db         14 SCAGSCTCKACRCPSCKKSCGCCCPVG 40

RESULT 9  
S00809  
metallothionein Ib - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: S00809  
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.  
Eur. J. Biochem. 174, 417-424, 1988  
A;Title: The sheep metallothionein gene family. Structure, sequence and evolutionary re  
A;Reference number: S00808; MUID:88254812; PMID:3383853  
A;Accession: S00809  
A:Molecule type: DNA  
A;Residues: 1-61 <PET>  
A;Cross-references: UNIPROT:P09577; EMBL:X07973; NID:gl338; PIDN:CAA30785.1; PID:gi339  
C;Genetics:  
A;Introns: 10/1; 32/1

C;Superfamily: metallothionein

Query Match 27.6%; Score 60; DB 2; Length 61;  
Best Local Similarity 44.4%; Pred. No. 3.3;  
Matches 12; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

QY 2 SCNG-VCSFPEPMPGCGTSACRIPVG 26  
|||  
Db 14 SCAGSTCKACRCPCSKKSCCPCPVG 40

## RESULT 10

MMRYS

laminin beta-2 chain precursor - rat  
N;Alternate names: laminin chain B3; S-laminin  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C;Accession: S03539

R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
A;Reference number: S03539; MUID:89159410; PMID:2922051  
A;Accession: S03539

A;Molecule type: mRNA  
A;Residues: 1-1801 <HUN>  
A;Cross-references: UNIPROT:P15800; EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F;1-35/Domain: signal sequence #status predicted <SIG>  
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>

F;36-285/Domain: VI <DOM6>  
F;286-555/Domain: V <DOM5>  
F;286-347/Domain: laminin-type EGF-like homology <LE01>  
F;350-410/Domain: laminin-type EGF-like homology <LE02>  
F;413-470/Domain: laminin-type EGF-like homology <LE03>  
F;473-522/Domain: laminin-type EGF-like homology <LE04>  
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;556-784/Domain: IV <DOM4>  
F;786-831/Domain: laminin-type EGF-like homology <LE06>  
F;788-1196/Domain: III <DOM3>  
F;834-877/Domain: laminin-type EGF-like homology <LE07>  
F;880-927/Domain: laminin-type EGF-like homology <LE08>  
F;930-986/Domain: laminin-type EGF-like homology <LE09>  
F;989-1038/Domain: laminin-type EGF-like homology <LE10>  
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F;1197-1412/Domain: II <DOM2>  
F;1197-1412/Region: heptad repeats  
F;1413-1445/Domain: alpha <ALP>  
F;1446-1801/Region: heptad repeats  
F;1446-1801/Domain: I <DOM1>  
F;45-50/Diulfide bonds: #status predicted  
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p  
F;1193,1196,1800/Diulfide bonds: interchain #status predicted

Query Match 26.7%; Score 58; DB 1; Length 1801;  
Best Local Similarity 41.7%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 14 PGTSAACRIPVGLVIGYCRNPSG 37  
|||  
Db 828 PAGCQACQSPDGAUSALCEGTSG 851

## RESULT 11

B48454

cathepsin B-like cysteine proteinase (EC 3.4.22.1) CP-3 - nematode (Ostertagia ostertagi)  
C;Species: Ostertagia ostertagi  
C;Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: B48454  
R;Pratt, D.; Boisvenue, R.J.; Cox, G.N.  
Mol. Biochem. Parasitol. 56, 39-48, 1992  
A;Title: Isolation of putative cysteine protease genes of Ostertagia ostertagi.  
A;Reference number: A48454; MUID:93116804; PMID:11475000  
A;Accession: B48454  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-174 <PRA>  
A;Cross-references: UNIPROT:Q06544; GB:M88505; NID:g159951; PIDN:AAA29436.1; PID:g159952  
A;Experimental source: larva  
A;Note: sequence extracted from NCBI backbone (NCBIN:121411, NCBI:P:124017)  
C;Superfamily: papain  
C;Keywords: cysteine proteinase; hydrolase; protein degradation

Query Match 26.3%; Score 57; DB 2; Length 174;  
Best Local Similarity 66.7%; Pred. No. 16;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GVCSPFEMPCCG 16  
|||  
Db 20 GCRDPVEFPCCG 31

## RESULT 12

WTFP

testis-specific protein (clone mst(3)gl-9) - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: S00340  
R;Kuhn, R.; Schaefer, U.; Schaefer, M.  
EMBO J. 7, 447-454, 1988

A;Title: Cis-acting regions sufficient for spermatocyte-specific transcriptional and spe  
A;Reference number: S00340; MUID:88211557; PMID:2835228  
A;Accession: S00340

A;Molecule type: DNA

A;Residues: 1-56 <KUH>

A;Cross-references: UNIPROT:P08175; EMBL:Y00831; NID:g8650; PIDN:CAA68761.1; PID:g8651

C;Genetics:

A;Gene: FlyBase:Mst87F

A;Cross-references: FlyBase:FBgn0002862

C;Superfamily: fruit fly testis-specific protein

C;Keywords: sex-specific protein; testis

Query Match 25.8%; Score 56; DB 1; Length 56;  
Best Local Similarity 38.2%; Pred. No. 8.7;  
Matches 13; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

QY 3 CNGVCSPFEMPCCGTSACRIPCIVGLVIGYCRNPS 36  
|||  
Db 2 CCGPCGPGCCGCGCCGCGCGCGPCYGN 35

## RESULT 13

A23889

metallothionein 1 - bovine (tentative sequence)

C;Species: Bos primigenius taurus (cattle)

C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 09-Jul-2004

C;Accession: A23889

R;Munger, K.; Germann, U.A.; Beltramini, M.; Niedermann, D.; Baitella-Eberle, G.; Kagi,

J. Biol. Chem. 260, 10032-10038, 1985

A;Title: (Cu,Zn)-metallothioneins from fetal bovine liver. Chemical and spectroscopic pro

A;Reference number: A92490; MUID:85261416; PMID:4019500

A;Accession: A23889

A;Molecule type: protein

A;Residues: 1-61 <MUN>

A;Cross-references: UNIPROT:P58280

C;Superfamily: metallothionein

Query Match 25.8%; Score 56; DB 2; Length 61;  
Best Local Similarity 44.0%; Pred. No. 9.3;  
Matches 11; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

Qy 2 SCNGVCSPPFEMPCCGTSACRCIPVG 26  
Db 18 SCK--CKACRCPCCKKSCCCCPVG 40

RESULT 14  
F71699  
diaminopimelate epimerase (dapF) RP415 - Rickettsia prowazekii  
C;Species: Rickettsia prowazekii  
C;Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
C;Accession: F71699  
R;Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alemark, U.  
Nature 396, 133-140, 1998  
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A;Reference number: A71630; MUID:99039499; PMID:9823893  
A;Accession: F71699  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-270 <AND>  
A;Cross-references: UNIPROT:Q9ZDB7; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA1487  
A;Experimental source: strain Madrid E  
C;Genetics:  
A;Gene: dapF; RP415  
C;Superfamily: diaminopimelate epimerase

Query Match 25.8%; Score 56; DB 2; Length 270;  
Best Local Similarity 40.9%; Pred. No. 28;  
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 15 CGTSACRCIPVGLVIGYCRNPS 36  
Db 213 CGSGACASFAAGLKLGFVHSPS 234

RESULT 15  
T16248  
hypothetical protein F35A5.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T16248  
R;Leimbach, D.  
submitted to the EMBL Data Library, January 1996  
A;Description: The sequence of C. elegans cosmid F35A5.  
A;Reference number: Z18495  
A;Accession: T16248  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-375 <LEI>  
A;Cross-references: UNIPROT:Q20002; EMBL:U46675; NID:g1166613; PID:g1166616; PIDN:AAB526  
A;Experimental source: strain Bristol N2; clone F35A5  
C;Genetics:  
A;Gene: CESP:F35A5.3  
A;Map position: X  
A;Introns: 14/3; 128/3; 187/3; 216/3; 246/3; 284/3  
C;Superfamily: gliadin

Query Match 25.8%; Score 56; DB 2; Length 375;  
Best Local Similarity 36.7%; Pred. No. 37;  
Matches 11; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

Qy 2 SCNGVCSPPFEMPCCGTS-----ACRCIPV 25  
Db 73 ACN--CAPVQDPCACOPQQQPCACNCAVP 100

RESULT 16  
I39383  
angio-associated migratory cell protein - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 16-Aug-2004  
C;Accession: I39383  
R;Beckner, M.E.; Kruttsch, H.C.; Stracke, M.L.; Williams, S.T.; Gallardo, J.A.; Liotta, Cancer Res. 55, 2140-2149, 1995

A;Title: Identification of a new immunoglobulin superfamily protein expressed in blood vessels  
A;Reference number: I39383; MUID:95262124; PMID:7743515  
A;Accession: I39383  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-452 <RES>  
A;Cross-references: UNIPROT:Q13685; GB:M95627; NID:g870802; PIDN:AAA68889.1; PID:g870803  
C;Genetics:  
A;Gene: GDB:AAMP  
A;Cross-references: GDB:4573993  
A;Map position: 14q32.1-14q32.1  
C;Superfamily: WD repeat homology  
F;148-181/Domain: WD repeat homology <WD1>  
F;414-447/Domain: WD repeat homology <WD2>

Query Match 25.8%; Score 56; DB 2; Length 452;  
Best Local Similarity 40.0%; Pred. No. 42;  
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

Qy 4 NGVCSPFEMPCCGTSACRCIPVG--LVIGY 31  
Db 223 NGDKTFQGNPCATCGRVLPDGKRAVVGY 252

RESULT 17  
T21192  
hypothetical protein F21C3.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T21192  
R;McMurray, A.  
submitted to the EMBL Data Library, April 1996  
A;Reference number: Z19388  
A;Accession: T21192  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-813 <WIL>  
A;Cross-references: UNIPROT:Q19673; EMBL:Z71261; PIDN:CAA95805.1; GSPDB:GN00019; CESP:F2  
A;Experimental source: clone F21C3  
C;Genetics:  
A;Gene: CESP:F21C3.2  
A;Map position: 1  
A;Introns: 39/1; 105/3; 175/3; 220/1; 294/3; 320/2; 345/3; 386/3; 443/3; 508/2; 635/1; 6

Query Match 25.8%; Score 56; DB 2; Length 813;  
Best Local Similarity 26.3%; Pred. No. 65;  
Matches 15; Conservative 7; Mismatches 15; Indels 20; Gaps 3;

Qy 1 ASCNG-----VCSPFEMP-----PCGTSAC-----RCIPVGLVIGYCRNPSG 37  
Db 676 ATCGGGGADSGISNPTTTPATNNGQNTPCDSPMCYNEDQCCFIWAQRGQCRSNPG 732

RESULT 18  
I48173  
metallothionein II - golden hamster  
C;Species: Mesocricetus auratus (golden hamster)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48173  
R;Duguid, J.R.; Rohwer, R.G.; Seed, B.  
Proc. Natl. Acad. Sci. U.S.A. 85, 5738-5742, 1988  
A;Title: Isolation of cDNAs of scrapie-modulated RNAs by subtractive hybridization of a  
A;Reference number: I48171; MUID:88289792; PMID:2456582  
A;Accession: I48173  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-61 <RES>  
A;Cross-references: UNIPROT:P17808; GB:J03848; NID:g191448; PIDN:AAA37101.1; PID:g305363  
C;Superfamily: metallothionein

Query Match 25.3%; Score 55; DB 2; Length 61;  
Best Local Similarity 44.4%; Pred. No. 12;  
Matches 12; Conservative 1; Mismatches 12; Indels 2; Gaps 1;



Search completed: March 28, 2005, 09:01:05  
Job time : 26.5 secs

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## OM protein - protein search, using sw model

Run on: March 28, 2005, 09:00:16 ; Search time 68.5 Seconds  
(without alignments)  
178.843 Million cell updates/sec

Title: US-09-674-496d-6

Perfect score: 217

Sequence: 1 ASNGVCSPEMPGCTGACRCIPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	88	40.6	18	11	US-09-782-130-12
4	86	39.6	101	15	US-10-424-599-269230
5	75	34.6	18	11	US-09-782-130-17
6	65	30.0	1024	16	US-10-408-765A-1481
7	65	30.0	1728	14	US-10-184-644-313
8	65	30.0	1728	14	US-10-184-634-313
9	65	30.0	1728	14	US-10-063-685-101
10	62	28.6	1798	9	US-09-845-583-8
11	60.5	27.9	2692	14	US-10-184-644-225
12	60.5	27.9	2692	14	US-10-184-634-225
13	60	27.6	1871	14	US-10-184-644-301

14	60	27.6	1871	14	US-10-184-634-301	Sequence 301, App
15	60	27.6	1871	14	US-10-063-685-91	Sequence 91, Appl
16	59.5	27.4	1355	14	US-10-123-155-421	Sequence 421, App
17	59.5	27.4	1355	14	US-10-146-731-421	Sequence 421, App
18	59.5	27.4	1355	14	US-10-140-472-421	Sequence 421, App
19	59.5	27.4	1355	14	US-10-141-761-421	Sequence 421, App
20	59.5	27.4	1355	14	US-10-142-885-421	Sequence 421, App
21	59.5	27.4	1355	14	US-10-158-790-421	Sequence 421, App
22	59.5	27.4	1355	15	US-10-137-871-421	Sequence 421, App
23	59.5	27.4	1355	15	US-10-140-923-421	Sequence 421, App
24	59.5	27.4	1355	15	US-10-141-756-421	Sequence 421, App
25	59.5	27.4	1355	15	US-10-141-759-421	Sequence 421, App
26	59.5	27.4	1355	15	US-10-140-805-421	Sequence 421, App
27	59.5	27.4	1355	15	US-10-140-864-421	Sequence 421, App
28	59.5	27.4	1355	15	US-10-142-426-421	Sequence 421, App
29	59	27.2	975	9	US-09-886-055-431	Sequence 431, App
30	59	27.2	1799	9	US-09-845-583-6	Sequence 6, Appli
31	58.5	27.0	1101	15	US-10-287-971-18	Sequence 18, Appl
32	58.5	27.0	1102	14	US-10-073-912-11	Sequence 11, Appl
33	58.5	27.0	3004	14	US-10-184-644-91	Sequence 91, Appl
34	58.5	27.0	3004	14	US-10-184-634-91	Sequence 91, Appl
35	58.5	27.0	3690	14	US-10-184-644-517	Sequence 517, App
36	58.5	27.0	3690	14	US-10-184-634-517	Sequence 517, App
37	58	26.7	413	13	US-10-087-192-519	Sequence 519, App
38	58	26.7	1801	9	US-09-938-275-8	Sequence 8, Appli
39	57.5	26.5	84	15	US-10-424-599-201814	Sequence 201814,
40	57.5	26.5	85	16	US-10-437-963-161069	Sequence 161069,
41	57.5	26.5	581	10	US-09-244-805-27	Sequence 27, Appl
42	57.5	26.5	581	10	US-09-245-277-27	Sequence 27, Appl
43	57.5	26.5	581	16	US-10-792-481-27	Sequence 28, Appl
44	57.5	26.5	7285	14	US-10-145-206-28	Sequence 40, Appl
45	57	26.3	67	14	US-10-087-887-40	Sequence 40, Appl
46	57	26.3	67	15	US-10-038-854-185	Sequence 185, App
47	57	26.3	101	15	US-10-424-599-158972	Sequence 158972,
48	57	26.3	101	15	US-10-425-114-49681	Sequence 49681, A
49	56.5	26.0	517	15	US-10-425-114-38947	Sequence 38947, A
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51	56	25.8	100	15	US-10-424-599-159634	Sequence 159634,
52	56	25.8	141	9	US-09-764-864-1489	Sequence 1489, Ap
53	56	25.8	371	16	US-10-437-963-146358	Sequence 146358,
54	56	25.8	452	16	US-10-789-378-2	Sequence 2, Appli
55	56	25.8	452	17	US-10-868-578A-24	Sequence 24, Appl
56	56	25.8	611	10	US-09-893-519A-28	Sequence 28, Appl
57	55.5	25.6	92	14	US-10-072-602B-219	Sequence 219, App
58	55.5	25.6	179	14	US-10-017-161-1510	Sequence 1510, Ap
59	55.5	25.6	708	14	US-10-184-644-211	Sequence 211, App
60	55.5	25.6	708	14	US-10-184-634-211	Sequence 211, App
61	55.5	25.6	1034	15	US-10-052-648A-31	Sequence 31, Appl
62	55.5	25.6	1034	15	US-10-052-648A-32	Sequence 32, Appl
63	55.5	25.6	1331	16	US-10-437-963-193234	Sequence 193234,
64	55.5	25.6	1730	14	US-10-123-155-7	Sequence 7, Appli
65	55.5	25.6	1730	14	US-10-146-731-7	Sequence 7, Appli
66	55.5	25.6	1730	14	US-10-140-472-7	Sequence 7, Appli
67	55.5	25.6	1730	14	US-10-141-761-7	Sequence 7, Appli
68	55.5	25.6	1730	14	US-10-142-885-7	Sequence 7, Appli
69	55.5	25.6	1730	14	US-10-158-790-7	Sequence 7, Appli
70	55.5	25.6	1730	15	US-10-137-871-7	Sequence 7, Appli
71	55.5	25.6	1730	15	US-10-140-923-7	Sequence 7, Appli
72	55.5	25.6	1730	15	US-10-141-756-7	Sequence 7, Appli
73	55.5	25.6	1730	15	US-10-141-759-7	Sequence 7, Appli
74	55.5	25.6	1730	15	US-10-140-805-7	Sequence 7, Appli
75	55.5	25.6	1730	15	US-10-140-864-7	Sequence 7, Appli
76	55.5	25.6	1730	15	US-10-142-426-7	Sequence 7, Appli
77	55	25.3	143	16	US-10-437-963-167377	Sequence 167377,
78	55	25.3	162	9	US-09-864-761-34582	Sequence 34582, A
79	55	25.3	301	16	US-10-437-963-167378	Sequence 167378,
80	55	25.3	364	16	US-10-437-963-139584	Sequence 139584,
81	55	25.3	377	16	US-10-437-963-154620	Sequence 154620,
82	55	25.3	397	16	US-10-437-963-154624	Sequence 154624,
83	55	25.3	691	16	US-10-437-963-119124	Sequence 119124,
84	55	25.3	1543	15	US-10-072-012-320	Sequence 320, App
85	55	25.3	1798	9	US-09-938-275-9	Sequence 9, Appli
86	55	25.3	2478	14	US-10-063-685-163	Sequence 163, App



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;
;
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 269230
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(101)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85135C.1.pep
; US-10-424-599-269230

Query Match      39.6%; Score 86; DB 15; Length 101;
Best Local Similarity 36.1%; Pred. No. 0.065;
Matches 13; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy      2 SCNGVCSFFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
Db      29 NCYGACIPXCHPCRSRXCRCVPXLTGTGFCIHTTG 64

RESULT 5
US-09-782-130-17
; Sequence 17, Application US/09782130
; Publication No. US20040055038A1
; GENERAL INFORMATION:
; APPLICANT: KNAUF, VIC C.
; APPLICANT: KRIDL, JEAN C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION
; TITLE OF INVENTION: AND EXPRESSION OF HETEROLOGOUS GENES
; FILE REFERENCE: 16518.052
; CURRENT APPLICATION NUMBER: US/09/782,130
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/232,861
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 08/812,665
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 08/484,941
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/105,852
; PRIOR FILING DATE: 1993-08-10
; PRIOR APPLICATION NUMBER: US 07/526,123
; PRIOR FILING DATE: 1990-05-21
; PRIOR APPLICATION NUMBER: US 07/267,685
; PRIOR FILING DATE: 1988-11-02
; PRIOR APPLICATION NUMBER: US 06/692,605
; PRIOR FILING DATE: 1985-01-17
; PRIOR APPLICATION NUMBER: US 07/582,241
; PRIOR FILING DATE: 1990-09-14
; PRIOR APPLICATION NUMBER: US 07/188,361
; PRIOR FILING DATE: 1988-04-29
; PRIOR APPLICATION NUMBER: US 07/168,190
; PRIOR FILING DATE: 1988-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protease
; OTHER INFORMATION: Inhibitor Palb peptide sequence
; US-09-782-130-17
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Query Match      34.6%; Score 75; DB 11; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.22;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      16 GTSACRCIPVGLVIGYCR 33
Db      1 GSPLCRCIPAGLVIGNCR 18

RESULT 6
US-10-408-765A-1481
; Sequence 1481, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1481
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-1481

Query Match      30.0%; Score 65; DB 16; Length 1024;
Best Local Similarity 34.1%; Pred. No. 80;
Matches 15; Conservative 4; Mismatches 15; Indels 10; Gaps 3;

Qy      2 SCNGVCSFFEMPPCG---TSACRC-----IPVGLVIG-YCRNP 35
Db      456 SCNLLCHPGPCPPCPAFMTKTCGGRTRHTVRCGQAVSVHCNSNP 499

RESULT 7
US-10-184-644-313
; Sequence 313, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Par, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 313
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-184-644-313
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RESULT 17  
US-10-146-731-421  
Sequence 421, Application US/10146731  
Publication No. US2003012962A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Garritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.

```

/ AFFILIATION: zhang, zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C168
/ CURRENT APPLICATION NUMBER: US/10/140,472
/ CURRENT FILING DATE: 2002-05-06
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 421
/ LENGTH: 1355
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-140-472-421

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RESULT 19  
US-10-141-761-421  
; Sequence 421, Application US/10141761



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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C153
; CURRENT APPLICATION NUMBER: US/10/137,871
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-871-421

Query Match      27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY      1  ASCNGVCSPPMPPCGTSACRCIPVGLVIGYCRNPSG 37
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Db      440  AACTG-CGTGAGCGGTGACCCAGGCTTGCGTGAAG 475

RESULT 23
US-10-140-923-421
; Sequence 421, Application US/10140923
; Publication No. US2003020735A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C188
; CURRENT APPLICATION NUMBER: US/10/140,923
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-923-421

Query Match      27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

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Db      440  AACTG-CGTGAGCGGTGACCCAGGCTTGCGTGAAG 475

RESULT 24
US-10-141-756-421
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; Sequence 421, Application US/10141756
; Publication No. US2003020735A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C200
; CURRENT APPLICATION NUMBER: US/10/141,756
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-756-421

Query Match      27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

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Db      440  AACTG-CGTGAGCGGTGACCCAGGCTTGCGTGAAG 475

RESULT 25
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; Sequence 421, Application US/10141759
; Publication No. US20030207361A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C197
; CURRENT APPLICATION NUMBER: US/10/141,759
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 421
; LENGTH: 1355
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:51:20 ; Search time 30 Seconds  
(without alignments)  
92.067 Million cell updates/sec

Title: US-09-674-496D-6  
Perfect score: 217  
Sequence: 1 ASNCVCSPEPMPGCTGACRCIPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	30.0	1073	4	US-09-949-016-9771
2	65	30.0	1104	2	US-08-327-832-5
3	65	30.0	1104	2	US-08-828-584-5
4	62	28.6	1798	4	US-09-845-583A-8
5	62	28.6	1798	4	US-09-561-709B-11
6	62	28.6	1798	4	US-09-917-254-87
7	61	28.1	291	4	US-09-902-540-15052
8	60.5	27.9	210	4	US-09-252-991A-20337
9	59	27.2	1799	4	US-09-845-583A-6
10	58.5	27.0	1101	4	US-09-561-709B-5
11	58.5	27.0	1761	4	US-09-561-709B-1
12	58	26.7	165	4	US-09-706-722A-10
13	57.5	26.5	581	4	US-09-244-805-27
14	56.5	26.0	998	4	US-09-252-991A-28424
15	56	25.8	41	3	US-08-836-686B-9
16	56	25.8	117	4	US-09-252-991A-17204
17	56	25.8	415	5	PCT-US93-00601-2
18	56	25.8	415	5	PCT-US94-07107A-2
19	56	25.8	425	5	PCT-US94-07107A-7
20	56	25.8	445	3	US-08-083-945C-2
21	55	25.3	445	3	US-08-083-945C-7
22	55	25.3	61	2	US-08-785-530-6
23	55	25.3	61	2	US-09-123-850-6
24	55	25.3	243	2	US-08-460-309-15
25	55	25.3	243	2	US-08-125-077-15
26	55	25.3	1854	4	US-09-949-016-11625
27	55	25.3	3075	2	US-08-460-309-5

28	55	25.3	3075	2	US-08-125-077-5	Sequence 5, Appli
29	54	24.9	64	4	US-09-270-767-59798	Sequence 59798, A
30	54	24.9	71	4	US-09-252-991A-20055	Sequence 20055, A
31	54	24.9	156	4	US-09-252-991A-22898	Sequence 22898, A
32	54	24.9	184	4	US-09-252-991A-25661	Sequence 25661, A
33	54	24.9	200	4	US-09-270-767-44372	Sequence 44372, A
34	53.5	24.7	2594	3	US-08-718-388-7	Sequence 7, Appli
35	53.5	24.7	5405	3	US-08-718-388-9	Sequence 9, Appli
36	53	24.4	37	3	US-08-836-686B-7	Sequence 7, Appli
37	53	24.4	75	4	US-09-489-039A-11668	Sequence 11668, A
38	53	24.4	254	4	US-09-586-106D-67	Sequence 67, Appli
39	53	24.4	3571	4	US-09-911-842A-2	Sequence 2, Appli
40	52.5	24.2	413	4	US-09-252-991A-23751	Sequence 23751, A
41	52.5	24.2	1754	1	US-07-745-206A-13	Sequence 13, Appli
42	52.5	24.2	1754	2	US-08-311-363-13	Sequence 13, Appli
43	52	24.0	41	3	US-08-836-686B-8	Sequence 8, Appli
44	52	24.0	400	2	US-08-103-170-9	Sequence 9, Appli
45	52	24.0	402	1	US-08-444-734A-6	Sequence 6, Appli
46	52	24.0	402	1	US-08-087-772A-15	Sequence 15, Appli
47	52	24.0	408	1	US-07-916-901-2	Sequence 2, Appli
48	52	24.0	408	1	US-08-351-473B-3	Sequence 3, Appli
49	52	24.0	408	3	US-08-450-962-2	Sequence 2, Appli
50	52	24.0	408	3	US-08-450-962-5	Sequence 5, Appli
51	52	24.0	408	4	US-08-848-631-2	Sequence 5, Appli
52	52	24.0	408	4	US-08-848-631-5	Sequence 5, Appli
53	52	24.0	1497	4	US-09-060-854B-2	Sequence 2, Appli
54	52	24.0	1497	4	US-09-529-904-3	Sequence 3, Appli
55	51.5	23.7	593	4	US-09-252-991A-23251	Sequence 23251, A
56	51.5	23.7	1342	4	US-09-561-709B-13	Sequence 13, Appli
57	51.5	23.7	1765	4	US-09-562-702A-16	Sequence 16, Appli
58	51.5	23.7	1765	4	US-09-561-818A-16	Sequence 16, Appli
59	51.5	23.7	1786	4	US-09-562-702A-14	Sequence 14, Appli
60	51.5	23.7	1786	4	US-09-561-818A-14	Sequence 14, Appli
61	51.5	23.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
62	51.5	23.7	1786	4	US-09-538-092-869	Sequence 869, App
63	51.5	23.7	4544	1	US-08-469-486-52	Sequence 52, Appli
64	51.5	23.7	4544	2	US-08-469-658-52	Sequence 52, Appli
65	51	23.5	137	4	US-09-489-039A-12891	Sequence 12891, A
66	51	23.5	243	2	US-08-460-309-16	Sequence 16, Appli
67	51	23.5	243	2	US-08-125-077-16	Sequence 16, Appli
68	51	23.5	281	4	US-09-248-796A-15282	Sequence 15282, A
69	51	23.5	344	1	US-08-689-974-1	Sequence 1, Appli
70	51	23.5	344	3	US-09-058-376-1	Sequence 1, Appli
71	51	23.5	690	4	US-09-371-338-19	Sequence 19, Appli
72	51	23.5	1652	4	US-09-627-650B-1	Sequence 1, Appli
73	51	23.5	1652	4	US-09-436-063C-1	Sequence 1, Appli
74	51	23.5	1917	4	US-09-627-650B-5	Sequence 5, Appli
75	51	23.5	1917	4	US-09-436-063C-5	Sequence 5, Appli
76	51	23.5	2508	4	US-09-627-650B-7	Sequence 7, Appli
77	51	23.5	2508	4	US-09-436-063C-7	Sequence 7, Appli
78	51	23.5	2544	4	US-09-627-650B-3	Sequence 3, Appli
79	51	23.5	2544	4	US-09-436-063C-3	Sequence 3, Appli
80	51	23.5	2601	4	US-09-627-650B-9	Sequence 9, Appli
81	51	23.5	2601	4	US-09-436-063C-9	Sequence 9, Appli
82	50.5	23.3	181	4	US-09-252-991A-23483	Sequence 23483, A
83	50.5	23.3	306	4	US-09-252-991A-23169	Sequence 23169, A
84	50.5	23.3	379	4	US-09-907-794A-4	Sequence 4, Appli
85	50.5	23.3	379	4	US-09-905-125A-4	Sequence 4, Appli
86	50.5	23.3	379	4	US-09-902-775A-4	Sequence 4, Appli
87	50.5	23.3	379	4	US-09-906-700-4	Sequence 4, Appli
88	50.5	23.3	379	4	US-09-903-603A-4	Sequence 4, Appli
89	50.5	23.3	379	4	US-09-904-520A-4	Sequence 4, Appli
90	50.5	23.3	379	4	US-09-909-064-4	Sequence 4, Appli
91	50.5	23.3	379	4	US-09-905-381A-4	Sequence 4, Appli
92	50.5	23.3	379	4	US-09-906-618-4	Sequence 4, Appli
93	50.5	23.3	380	4	US-09-205-258-441	Sequence 441, App
94	50	23.0	50	3	US-08-836-686B-4	Sequence 4, Appli
95	50	23.0	50	3	US-08-836-686B-6	Sequence 6, Appli
96	50	23.0	51	3	US-08-836-686B-2	Sequence 2, Appli
97	50	23.0	61	2	US-08-785-530-1	Sequence 1, Appli
98	50	23.0	61	2	US-09-123-850-1	Sequence 1, Appli
99	50	23.0	61	4	US-09-949-016-6675	Sequence 6675, Ap
100	50	23.0	108	4	US-09-270-767-46529	Sequence 46529, A





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Best Local Similarity 57.7%; Pred. No. 13;
Matches 15; Conservative 1; Mismatches 7; Indels 3; Gaps 2;

QY 1 ASCNGVCSPPFMPGCGTSACRCIPVG 26
Db 106 ASCSTTCS--TPPPCG-SACRDWPSG 128

RESULT 9
US-09-845-583A-6
; Sequence 6, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845.583A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-6

Query Match 27.2%; Score 59; DB 4; Length 1799;
Best Local Similarity 35.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 6 VCSPP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37
Db 816 VCATGYGFGPGACQACQCSPDGALSALCBGTSG 849

RESULT 10
US-09-561-709B-5
; Sequence 5, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-5

Query Match 27.0%; Score 58.5; DB 4; Length 1101;
Best Local Similarity 41.9%; Pred. No. 1e+02;
Matches 18; Conservative 2; Mismatches 10; Indels 13; Gaps 4;

QY 2 SC--NGVCSPPFMPGCG-----TSACRCIP--VGLVIGYC 32
Db 1023 SCHASGV-SPMECPGCGGACLCDPVTGACPCLEPNVTGLACDRC 1064

RESULT 11
US-09-561-709B-1
; Sequence 1, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-1

Query Match 27.0%; Score 58.5; DB 4; Length 1761;
Best Local Similarity 41.9%; Pred. No. 1.6e+02;
Matches 18; Conservative 2; Mismatches 10; Indels 13; Gaps 4;

QY 2 SC--NGVCSPPFMPGCG-----TSACRCIP--VGLVIGYC 32
Db 1023 SCHASGV-SPMECPGCGGACLCDPVTGACPCLEPNVTGLACDRC 1064

RESULT 12
US-09-706-722A-10
; Sequence 10, Application US/09706722A
; Patent No. 6670328
; GENERAL INFORMATION:
; APPLICANT: LASSALLE, PHILIPPE
; APPLICANT: MARCHANDISE, GENEVIEVE
; APPLICANT: KEROVAZE, GWENOLA
; APPLICANT: TONNEL, ANDRE BERNARD
; APPLICANT: MOLLET, SOPHIE
; TITLE OF INVENTION: PROTEINS AND PETIDES DERIVED FROM PROTEIN ESM-1 AND
; THEIR USES IN THE TREATMENT AND DIAGNOSIS OF DISEASES
; FILE REFERENCE: 8425/P-61263US2
; CURRENT APPLICATION NUMBER: US/09/706,722A
; CURRENT FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/102,909
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/050,614
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Laminin B2 (lmb2)
; OTHER INFORMATION: amino acid sequence
US-09-706-722A-10

Query Match 26.7%; Score 58; DB 4; Length 165;
Best Local Similarity 41.7%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 14 PGTSACRCIPVGLVIGYCRNPSG 37
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RESULT 15
US-08-836-686B-9
; Sequence 9, Application US/08836686B
; Patent No. 6239106
; GENERAL INFORMATION:
; APPLICANT: Voerman, Gerard
; TITLE OF INVENTION: A novel family of protease inhibitors, and other
; TITLE OF INVENTION: biologic active substances
; FILE REFERENCE: 70140
; CURRENT APPLICATION NUMBER: US/08/836,686B
; CURRENT FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: EPO 94117053.2
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EPO 95103637.5
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/EP95/04223
; PRIOR FILING DATE: 1995-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Limnatis nilotica
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(41)
; OTHER INFORMATION: sequence of another isoform, which was found to be
; OTHER INFORMATION: a mixture of two molecules, in peak 9 (figure 7)
US-08-836-686B-9

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RESULT 15
US-08-836-686B-9
; Sequence 9, Application US/08836686B
; Patent No. 6239106
; GENERAL INFORMATION:
; APPLICANT: Voerman, Gerard
; TITLE OF INVENTION: A novel family of protease inhibitors, and other
; TITLE OF INVENTION: biologic active substances
; FILE REFERENCE: 70140
; CURRENT APPLICATION NUMBER: US/08/836,686B
; CURRENT FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: EPO 94117053.2
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EPO 95103637.5
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/EP95/04223
; PRIOR FILING DATE: 1995-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Limnatis nilotica
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(41)
; OTHER INFORMATION: sequence of another isoform, which was found to be
; OTHER INFORMATION: a mixture of two molecules, in peak 9 (figure 7)
US-08-836-686B-9

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; Sequence 9, Application US/08836686B
; Patent No. 6239106
; GENERAL INFORMATION:
; APPLICANT: Voerman, Gerard
; TITLE OF INVENTION: A novel family of protease inhibitors, and other
; TITLE OF INVENTION: Biologic active substances
; FILE REFERENCE: 70140
; CURRENT APPLICATION NUMBER: US/08/836.686B
; CURRENT FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: EPO 94117053.2
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EPO 95103637.5
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/EP95/04223
; PRIOR FILING DATE: 1995-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Limnatis nilotica
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(41)
; OTHER INFORMATION: sequence of another isoform, which was found to be
; - OTHER INFORMATION: a mixture of two molecules, in peak 9 (figure 7)
US-08-836-686B-9

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Matches 13; Conservative 6; Mismatches 11; Indels 4; Gaps 4

DB 3 NCGGQVCSKGL--CVDGQCKCTPIRCLT-YCPN 33

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; Sequence 17204, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17204
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-17204

Query Match 25.8%; Score 56; DB 4; Length 117;
Best Local Similarity 36.78; Pred. No. 23;

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Matches 11; Conservative 3; Mismatched 8; Index 8; Garbled 8

DB / CSPAPACATSSSICC-----CASPT 28

RESULT 17  
PCT-US93-00601-2

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; Sequence 2, Application PC/TUS9300601
;
; GENERAL INFORMATION:
; APPLICANT: Beckner, Marie E.
; APPLICANT: Liotta, Lance A.
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00601
; FILING DATE: 19930129
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-00601-2

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Query Match	25.8%;	Score 56;	DB 5;	Length 415;
Best Local Similarity	40.0%;	Pred.No. 77;		
Matches 12;	Conservative 4;	Mismatches 12;	Indels 2;	Gaps 1;
Qy	4	NGVCSPFEMPCCGTACRCIPVG--LVIGY	31	
Db	205	NGDCKTFQGNCPATCGRLVDPGKRAVVGY	234	

RESULT 18  
PCT-US94-071107A-2  
Sequence 2, Application PC/TUS9407107A  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of  
America, as represented by the Secretary/  
APPLICANT: Department of Health and Human Services  
TITLE OF INVENTION: AAMP-1  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07107A  
FILING DATE: 25-JUN-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,043  
FILING DATE: 29-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684

```

; REFERENCE/DOCKET NUMBER: 15280-156-1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07107A-2

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Query Match 25.8%; Score 56; DB 5; Length 415;  
Best Local Similarity 40.0%; Pred. No. 77;  
Matches 12; Conservative 4; Mismatches 12; Indels

QY 4 NGVCSPEMPPPCGTSACRCIPVG--LVIGY 31  
||| ||| : | : | : |||  
Db 205 NGDKTFOGPNCPATCGRVLDPDGKRAVVG 234  
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RESULT 19
PCT-US94-07107A-7
; Sequence 7, Application PC/TUS9407107A
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of
; APPLICANT: America, as represented by the Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07107A  
FILING DATE: 25-JUN-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,043  
FILING DATE: 29-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 15280-156-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-07107A-7

Query Match 25.8%; Score 56; DB 5; Length 426;  
Best Local Similarity 40.0%; Pred. No. 79;  
Matches 12: Conservative 4; Mismatches 12: Indels

QY            4 NGVCSPFEMPFCGTSACRCIPVG--LVIGY 31  
             ||| | : | : | : | : | : | :  
Db          216 NGDCKTFOGNCPATCGRVLDPGRVAVGY 245



RESULT 20  
US-08-083-945C-2  
; Sequence 2, Application US/08083945C  
; Patent No. 6274134  
; GENERAL INFORMATION:  
; APPLICANT: Beckner, Marie E.  
; APPLICANT: Liotta, Lance A.  
; APPLICANT: Kruttsch, Henry C.  
; TITLE OF INVENTION: AAMP-1  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/083,945C  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,043  
; FILING DATE: 29-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 15280-156-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-083-945C-2

Query Match 25.8%; Score 56; DB 3; Length 445;  
Best Local Similarity 40.0%; Pred. No. 82;  
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;  
Qy 4 NGVSPFEMPCCGTSACRCIPVG--LVIGY 31  
Db 216 NGDCKTFQGNPCATCGRVLPDGRVAVGY 245

RESULT 21  
US-08-083-945C-7  
; Sequence 7, Application US/08083945C  
; Patent No. 6274134  
; GENERAL INFORMATION:  
; APPLICANT: Beckner, Marie E.  
; APPLICANT: Liotta, Lance A.  
; APPLICANT: Kruttsch, Henry C.  
; TITLE OF INVENTION: AAMP-1  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/083,945C  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,043  
; FILING DATE: 29-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 15280-156-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-083-945C-7

Query Match 25.8%; Score 56; DB 3; Length 445;  
Best Local Similarity 40.0%; Pred. No. 82;  
Matches 12; Conservative 4; Mismatches 12; Indels 2; Gaps 1;  
Qy 4 NGVSPFEMPCCGTSACRCIPVG--LVIGY 31  
Db 216 NGDCKTFQGNPCATCGRVLPDGRVAVGY 245

RESULT 22  
US-08-785-530-6  
; Sequence 6, Application US/08785530  
; Patent No. 5814480  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/785,530  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0194 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 305363  
US-08-785-530-6

Query Match 25.3%; Score 55; DB 2; Length 61;  
Best Local Similarity 44.4%; Pred. No. 16;  
Matches 12; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 2 SCNGVCSPPF--MPPCGTSACRCIPVG 26  
Db 14 SCGSGCKCKCKCTTCKKSCCSCCPVG 40

RESULT 23  
US-09-123-850-6  
; Sequence 6, Application US/09123850  
; Patent No. 5955428  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/123,850  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/785,530  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0194 US  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 305363  
US-09-123-850-6

Query Match 25.3%; Score 55; DB 2; Length 61;  
Best Local Similarity 44.4%; Pred. No. 16;  
Matches 12; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 2 SCNGVCSPPF--MPPCGTSACRCIPVG 26  
Db 14 SCGSGCKCKCKCTTCKKSCCSCCPVG 40

## RESULT 24

US-08-460-309-15  
; Sequence 15, Application US/08460309  
; Patent No. 5837496  
; GENERAL INFORMATION:  
; APPLICANT: Engvall, Eva  
; APPLICANT: Leivo, Ilmo  
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
; TITLE OF INVENTION: Fragments and Uses Thereof  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,309  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,077  
; FILING DATE: 22-SEP-1993  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,309  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,077  
; FILING DATE: 22-SEP-1993  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,309  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,077  
; FILING DATE: 22-SEP-1993  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,309  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,077  
; FILING DATE: 22-SEP-1993  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,309  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,077  
; FILING DATE: 22-SEP-1993  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994

Qy 8 SPFMPGTSACRCIPVGLVIGYC 32  
Db 118 SPYEDEPC--RPCNCDPVGSLSSVC 140

## RESULT 25

US-08-125-077-15  
; Sequence 15, Application US/08125077  
; Patent No. 5872231  
; Patent No. 5872231 5840863  
; GENERAL INFORMATION:  
; APPLICANT: Engvall, Eva  
; APPLICANT: Leivo, Ilmo  
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
; TITLE OF INVENTION: Fragments and Uses Thereof  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,077  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-125-077-15

Query Match 25.3%; Score 55; DB 2; Length 243;  
Best Local Similarity 44.0%; Pred. NO. 60;  
Matches 11; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 8 SPFEMPCCGTSACRCIPVGLVIGVC 32  
Db 118 SPYEDEPC--RPCNCDPVGLSSVC 140

Search completed: March 28, 2005, 09:02:15  
Job time : 31 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:39:59 ; Search time 92 Seconds  
(without alignments)  
155.545 Million cell updates/sec

Title: US-09-674-496d-6  
Perfect score: 217  
Sequence: 1 ASCNGVCSPEMPGCTGACRCIPVGLVIGYCRNPSG 37

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	100.0	37	3	AY55990 Insectici
2	216	99.5	37	3	AY55991 Insectici
3	154	71.0	37	3	AY55992 Insectici
4	88	40.6	18	4	AAB85936 PA1b seed
5	88	40.6	18	8	ADO21580 Pea album
6	75	34.6	18	4	AAB85941 PA1b seed
7	75	34.6	18	8	ADO21585 Pea album
8	65	30.0	1024	5	ABB05595 Human nuc
9	62	28.6	1024	7	ADJ69675 Human hea
10	65	30.0	1104	2	AAR94957 NF-X1 DNA
11	63	29.0	838	4	ABB64668 Drosophil
12	62	28.8	564	8	ADP29241 Human sec
13	62	28.6	582	4	AAM51816 Murine ap
14	62	28.6	1798	5	AAM84346 Protein L
15	62	28.6	1798	5	AAM50360 Human lam
16	61	28.1	94	3	AAG08039 Arabidops
17	61	28.1	94	3	AAG37331 Arabidops
18	61	28.1	96	3	AAG08038 Arabidops
19	61	28.1	96	3	AAG37330 Arabidops
20	61	28.1	114	3	AAG08037 Arabidops
21	61	28.1	114	3	AAG37329 Arabidops
22	60.5	27.9	210	7	ABO71791 Pseudomon
23	60.5	27.9	681	8	ADP30850 Human sec
24	60.5	27.9	915	8	ADP30957 Human sec
25	59.5	27.4	576	8	ADP29284 Human sec

26	59	27.2	1799	5	AAM50359	Mouse lam
27	59	27.2	1799	8	ADS17495	Adri17495 Amino aci
28	59	27.2	1799	8	ADR97664	ADR97664 Murine la
29	58.5	27.0	885	7	ADE08939	Novel pro
30	58.5	27.0	1029	8	ADN04730	Antipeori
31	58.5	27.0	1101	7	ADE28641	Human NOV
32	58.5	27.0	1101	8	ADM93386	Human NOV
33	58.5	27.0	1105	2	AAI15459	SEQ ID 5
34	58.5	27.0	1670	7	ADE07851	Novel lam
35	58.5	27.0	1761	2	AAI15457	Human lam
36	58	26.7	165	8	ADM24888	Laminin b
37	58	26.7	413	7	ABM85368	Mouse pro
38	58	26.7	1801	2	AAM50895	Rat lamin
39	58	26.7	1801	7	ADE60383	Rat Prote
40	57.5	26.5	581	2	AAI42774	Rat neuro
41	57.5	26.5	581	4	AAM51819	Novel pro
42	57.5	26.5	7285	6	ABJ38280	PAMG21-RA
43	57	26.3	152	2	AAR12094	Antigenic
44	57	26.3	174	2	AAR12095	Antigenic
45	57	26.3	1579	4	ABBS8902	Drosophil
46	57	26.3	4360	8	ADP30525	Human sec
47	56.5	26.0	152	2	AAR24045	Apolipop
48	56.5	26.0	271	7	ADJ92151	Human hai
49	56.5	26.0	998	7	ABO79678	Pseudomon
50	56	25.8	56	4	ABB66566	Drosophil
51	56	25.8	117	7	ABO68458	Pseudomon
52	56	25.8	141	4	AAU16536	Human nov
53	56	25.8	141	6	ABU55605	Human nov
54	56	25.8	377	4	ABB68017	Drosophil
55	56	25.8	415	2	AAR32922	AAMP-1
56	56	25.8	415	2	AAR66773	N-termina
57	56	25.8	426	2	AAR66776	Cell adhe
58	56	25.8	452	8	ABM80393	Tumour-as
59	56	25.8	452	8	ADR73434	Human ang
60	56	25.8	611	5	AAU82968	Human hom
61	55.5	25.6	92	5	ABG99510	Conus sp
62	55.5	25.6	137	4	AAU45020	Propionib
63	55.5	25.6	137	6	ABM41539	Propionib
64	55.5	25.6	238	7	ABM74267	DNA clone
65	55.5	25.6	318	4	AAG71666	Human olf
66	55.5	25.6	318	4	AAG72405	Human OR-
67	55.5	25.6	976	8	ADP30688	Human sec
68	55.5	25.6	1676	8	ADP30515	Human sec
69	55	25.3	42	4	ADG27736	Human nov
70	55	25.3	76	4	AAU66727	Propionib
71	55	25.3	76	4	AAU52006	Propionib
72	55	25.3	76	6	ABM48525	Propionib
73	55	25.3	76	6	ABM63246	Propionib
74	55	25.3	142	4	AAU33434	Propionib
75	55	25.3	142	6	ABM49953	Propionib
76	55	25.3	162	4	AAU14874	Peptide #
77	55	25.3	162	4	ABB33842	Peptide #
78	55	25.3	162	4	AAU27301	Peptide #
79	55	25.3	162	4	ABB28658	Peptide #
80	55	25.3	162	4	ABBI9284	Protein #
81	55	25.3	162	4	AAU67014	Human bon
82	55	25.3	162	4	AAU54608	Human bra
83	55	25.3	162	4	ABG48677	Human liv
84	55	25.3	162	4	AAU02599	Peptide #
85	55	25.3	162	5	ABG36671	Human pep
86	55	25.3	171	6	ABU70429	Human adi
87	55	25.3	642	4	AAU00786	Human bon
88	55	25.3	1216	4	ABG09754	Novel hum
89	55	25.3	1543	5	AD116784	Human NOV
90	55	25.3	1543	8	ADN42438	Human nov
91	55	25.3	1555	7	ADC39156	Novel hum
92	55	25.3	1566	8	ADH72284	Human pro
93	55	25.3	1566	7	ADC39166	Novel hum
94	55	25.3	1789	8	ADH72294	Human pro
95	55	25.3	1789	8	ADP31028	Human sec
96	55	25.3	1798	2	AAW50896	Human lam
97	55	25.3	1798	7	ADE60385	Human pro
98	55	25.3	2901	4	ABG09763	Novel hum



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PN WO959695-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-FR001085.
XX
XX 11-MAY-1998; 98FR-00005877.
XX
XX (NASC-) INST NAT SCI APPLIQUEES LYON.
PA (INRG) INST NAT RECH AGRONOMIQUE.
XX
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;
XX
XX WPI; 2000-062304/05.
XX
XX Use of polypeptide as insecticide, especially for controlling cereal
PT grain pests.
XX
XX Example 2; Fig 7; 38pp; French.
XX
XX This sequence represents the Cys-rich peptide sequence of legume plant
CC derived insecticidal peptide leginsuline corresponding to that of an
CC entomotoxic pea protein. The invention relates to a novel insecticidal
CC peptide PT (AAV55990) isolated from pea plants which has homology to the
CC Palb peptide (AAV55991) and to the leginsuline from soybeans. The
CC insecticidal peptides preferably have the amino acid sequence:
CC X1CysX2CysX3CysX4CysX5CysX6CysX7, where X1 = 2-10 amino acids; X2 = 2-5
CC amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
CC acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
CC peptides can be used to protect cereal products or plants from attack by
CC cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
CC Acyrthosiphon pisum, either directly or by genetically modifying plants
CC (especially cereal plants) to express the peptide in their tissues or
CC organs
XX
XX Sequence 37 AA;
SQ
Query Match 71.0%; Score 154; DB 3; Length 37;
Best Local Similarity 59.5%; Pred. No. 2.8e-09;
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 ASCNGVCSPPFEMPCCGTSGACRCIPVGLVIGYCRNPSSG 37
DB 1 ADCNGACSPFPPVPCRSRDCRCVPIGLVFGVCFIHTPG 37
RESULT 4
AAB85936
ID AAB85936 standard; peptide; 18 AA.
XX
XX AAB85936;
XX
XX 30-NOV-2001 (first entry)
XX
XX Palb seed storage protein fragment.
XX
XX Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
KW 2A11; PA1B.
XX
XX Unidentified.
OS
XX US6281410-B1.
XX
XX 28-AUG-2001.
XX
XX 15-JAN-1999; 99US-00232861.
XX
XX 31-JUL-1986; 86US-00891529.
XX
XX 26-MAY-1987; 87US-00054369.
PR 28-JUL-1987; 87US-00078538.
PR 25-JAN-1988; 88US-00147781.
PR 15-MAR-1988; 88US-00168190.
PR 29-APR-1988; 88US-00188361.
PR

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PR 02-NOV-1988; 88US-00267685.
PR 21-MAY-1990; 90US-00526123.
PR 09-JUL-1990; 90US-00550804.
PR 10-AUG-1993; 93US-00105852.
PR 07-JUN-1995; 95US-00484941.
PR 07-MAR-1997; 97US-00812665.
XX
XX (CALJ) CALGENE LLC.
PA
XX Knauf VC, Kridl JC;
XX
XX WPI; 2001-564354/63.
XX
XX Obtaining a plant that produces a seed with a modified phenotype or
PT altering a seed phenotype, comprises transforming a plant cell with a DNA
PT construct consisting of operably linked components in the direction of
PT transcription.
XX
XX Example 9; Fig 6; 68pp; English.
XX
XX The invention provides a method for obtaining a plant which produces at
CC least one seed having a modified phenotype. The method involves
CC transforming a host plant cell with a DNA construct which consists of
CC operably linked components in the direction of transcription, a promoter
CC region from a Brassica plant gene, a DNA sequence of interest other than
CC the native coding sequence, and a transcription termination region. The
CC method is useful for obtaining plants having modified phenotype or for
CC altering the phenotype of a plant seed or tissue. The DNA constructs are
CC used in manipulating plant cells to provide for regulated transcription,
CC such as light inducible transcription, in a plant tissue or plant part of
CC interest at particular stages of plant growth or in response to external
CC control. These constructs are also used for modulation of expression of
CC endogenous products as well as production of exogenous products in the
CC seed. Sequences AAB85936-39 represent fragments of storage proteins used
CC in comparison studies with the storage protein 2A11
XX
XX Sequence 18 AA;
SQ
Query Match 40.6%; Score 88; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.015;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 6 VCSPPFEMPCCGTSGACRCI 23
DB 1 VCSPPFDIPCCGPLCRCI 18
RESULT 5
ADO21580
ID ADO21580 standard; peptide; 18 AA.
XX
XX ADO21580;
XX
XX 01-JUL-2004 (first entry)
XX
XX Pea albumin 1b reactive site.
DE
XX Pea; fruit specific promoter; plant; transgenic; protein storage;
KW improved nutrient source; enhanced response to light;
KW dehydration resistance; herbicide resistance; pest resistance; 2A11 gene;
KW protease inhibitor.
XX
XX Pisum sativum.
OS
XX US2004055038-A1.
XX
XX 18-MAR-2004.
XX
XX 12-FEB-2001; 2001US-00782130.
XX
XX 17-JAN-1985; 85US-00692605.
PR 31-JUL-1986; 86US-00891529.
PR 26-MAY-1987; 87US-00054369.
PR

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28-JUL-1987; 87US-00078538.  
25-JAN-1988; 88US-00147781.  
15-MAR-1988; 88US-00168190.  
29-APR-1988; 88US-00183361.  
02-NOV-1988; 88US-00267685.  
21-MAY-1990; 90US-00526123.  
09-JUL-1990; 90US-00550804.  
14-SEP-1990; 90US-00582241.  
08-AUG-1991; 91US-00742834.  
10-AUG-1993; 93US-00105852.  
07-JUN-1995; 95US-00484941.  
07-MAR-1997; 97US-00812665.  
15-JAN-1999; 99US-00232861.  
  
(KNAU/) KNAUF V C.  
(KRIDL/) KRIDL J C.  
  
Knauf VC, Kridl JC;  
  
WPI; 2004-247819/23.  
  
New DNA construct comprising a promoter region, a DNA sequence of interest and a transcription termination region, useful for producing transgenic plants.  
  
Example 9; Fig 6; 68pp; English.  
  
The invention relates to a DNA construct comprising, as operably linked components in the direction of transcription, a promoter region obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier protein (ACP) gene, a DNA sequence of interest other than the native coding sequence of the gene and a transcription termination region, where the components are functional in a plant cell and where the DNA construct is flanked by T-DNA. Also included are a plant cell having an altered phenotype as a result of expression of a DNA construct, a plant comprising cells comprising a DNA construct, a seed obtained from the plant, obtaining a plant having a modified phenotype or modifying the genotype of a plant to impart a desired characteristic to seed as distinct from other plant tissue, altering the phenotype of plant seed tissue or modifying transcription in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue. The DNA construct is useful in modifying or altering the genotype or phenotype of a plant to impart a desired characteristic. The construct is also useful in regulating specific transcription and expression in plants. The plants produced have increased capability of protein storage, improved nutrient source, enhanced response to light and dehydration resistance and resistant to herbicide and pests. The seed specific promoters are from the Napin, ACP and EA9 genes and the fruit specific promoter is from the tomato 2A11 gene. The present sequence is a reactive site from a protein similar to the tomato 2A11 protein (thought to be a protease inhibitor).  
  
Sequence 18 AA;  
  
Query Match 40.6%; Score 88; DB 8; Length 18;  
Best Local Similarity 72.2%; Pred. No. 0.015;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 6 VCSPPFPPCCTGTSACRCI 23  
Db 1 VCSPPFDIPPCGSLCRCI 18  
  
RESULT 6  
AAB85941  
ID AAB85941 standard; peptide; 18 AA.  
XX AC AAB85941;  
XX AC AAB85941;  
DT 30-NOV-2001 (first entry)  
XX PA1b seed storage protein fragment.

XX Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;  
KW 2A11; PALB.  
XX Unidentified.  
XX US6281410-B1.  
PD 28-AUG-2001.  
XX 15-JAN-1999; 99US-00232861.  
XX 31-JUL-1986; 86US-00891529.  
PR 26-MAY-1987; 87US-00054369.  
PR 28-JUL-1987; 87US-00078538.  
PR 25-JAN-1988; 88US-00147781.  
PR 15-MAR-1988; 88US-00168190.  
PR 29-APR-1988; 88US-00188361.  
PR 02-NOV-1988; 88US-00267685.  
PR 21-MAY-1990; 90US-00526123.  
PR 09-JUL-1990; 90US-00550804.  
PR 10-AUG-1993; 93US-00105852.  
PR 07-JUN-1995; 95US-00484941.  
PR 07-MAR-1997; 97US-00812665.  
XX (CALJ ) CALGENE LLC.  
XX Knauf VC, Kridl JC;  
XX WPI; 2001-564354/63.  
XX Obtaining a plant that produces a seed with a modified phenotype or altering a seed phenotype, comprises transforming a plant cell with a DNA construct consisting of operably linked components in the direction of transcription.  
XX Example 9; Fig 6; 68pp; English.  
XX The invention provides a method for obtaining a plant which produces at least one seed having a modified phenotype. The method involves transforming a host plant cell with a DNA construct which consists of operably linked components in the direction of transcription, a promoter region from a Brassica plant gene, a DNA sequence of interest other than the native coding sequence, and a transcription termination region. The method is useful for obtaining plants having modified phenotype or for altering the phenotype of a plant seed or tissue. The DNA constructs are used in manipulating plant cells to provide for regulated transcription, such as light inducible transcription, in a plant tissue or plant part of interest at particular stages of plant growth or in response to external control. These constructs are also used for modulation of expression of endogenous products as well as production of exogenous products in the seed. Sequences AAB85941-47 represent fragments of storage proteins used in comparison studies with the storage protein 2A11  
XX Sequence 18 AA;  
Query Match 34.6%; Score 75; DB 4; Length 18;  
Best Local Similarity 72.2%; Pred. No. 0.35;  
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 16 GTSACRCIPVGLVIGYCR 33  
Db 1 GSPLCRCIPAGLVIGNCR 18  
  
RESULT 7  
ADO21585  
ID ADO21585 standard; peptide; 18 AA.  
XX AC ADO21585;  
XX AC ADO21585;  
DT 01-JUL-2004 (first entry)  
XX



DE Pea albumin 1b N-terminus.

XX Pea; fruit specific promoter; plant; transgenic; protein storage;

KW improved nutrient source; enhanced response to light;

KW dehydration resistance; herbicide resistance; pest resistance; 2A11 gene;

XX protease inhibitor.

XX Pisum sativum.

OS

XX US2004055038-A1.

XX 18-MAR-2004.

XX

XX 12-FEB-2001; 2001US-00782130.

XX

XX 17-JAN-1985; 85US-00692605.

PR 31-JUL-1986; 86US-00891529.

PR 26-MAY-1987; 87US-00054369.

PR 28-JUL-1987; 87US-00078538.

PR 25-JAN-1988; 88US-0047781.

PR 15-MAR-1988; 88US-00168190.

PR 29-APR-1988; 88US-00188361.

PR 02-NOV-1988; 88US-00267685.

PR 21-MAY-1990; 90US-00526123.

PR 09-JUL-1990; 90US-00550804.

PR 14-SEP-1990; 90US-00582241.

PR 08-AUG-1991; 91US-00742834.

PR 10-AUG-1993; 93US-00105852.

PR 07-JUN-1995; 95US-00484941.

PR 07-MAR-1997; 97US-00812665.

PR 15-JAN-1999; 99US-00232861.

XX (KNAU//) KNAUF V C.

PA (KRIDL//) KRIDL J C.

XX

XX Knauf VC, Kridl JC;

XX

XX WPI; 2004-247819/23.

XX

XX New DNA construct comprising a promoter region, a DNA sequence of interest and a transcription termination region, useful for producing transgenic plants.

XX

XX Example 9; Fig 6; 68pp; English.

XX

XX The invention relates to a DNA construct comprising, as operably linked components in the direction of transcription, a promoter region obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier protein (ACP) gene, a DNA sequence of interest other than the native coding sequence of the gene and a transcription termination region, where the components are functional in a plant cell and where the DNA construct is flanked by T-DNA. Also included are a plant cell having an altered phenotype as a result of expression of a DNA construct, a plant comprising cells comprising a DNA construct, a seed obtained from the plant, obtaining a plant having a modified phenotype or modifying the genotype of a plant to impart a desired characteristic to seed as distinct from other plant tissue, altering the phenotype of plant seed tissue or modifying transcription in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue. The DNA construct is useful in modifying or altering the genotype or phenotype of a plant to impart a desired characteristic. The construct is also useful in regulating genetic modification of plant or regulating tissue and/or developmental specific transcription and expression in plants. The plants produced have increased capability of protein storage, improved nutrient source, enhanced response to light and dehydration resistance and resistant to herbicide and pests. The seed specific promoters are from the Napin, ACP and EA9 genes and the fruit specific promoter is from the tomato 2A11 gene. The present sequence is the N-terminus from a protein similar to the tomato 2A11 protein (thought to be a protease inhibitor).

XX Sequence 18 AA;

SQ

Query Match 34.6%; Score 75; DB 8; Length 18;  
Best Local Similarity 72.2%; Pred. No. 0.35;  
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 16 GTSACRCIPVGLVIGYCR 33  
: ||||| ||||| ||  
Db 1 GSPLCRCIPAGLVIGNCR 18

RESULT 8  
ABB05595  
ID ABB05595 standard; protein; 1024 AA.  
XX  
AC ABB05595;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE Human nuclear transcription factor 2 (NFX2) protein.  
XX  
KW Human; nuclear transcription factor 2; NFX2; chromosome 9; gene therapy.  
XX  
OS Homo sapiens.  
XX CN1318556-A.  
XX  
PD 24-OCT-2001.  
XX  
PF 11-APR-2001; 2001CN-00113502.  
XX  
PR 11-APR-2001; 2001CN-00113502.  
XX  
PA (UYNA-) UNIV NANJING MEDICAL.  
XX  
XX Sha J, Zhou Z, Li J;  
XX  
XX WPI; 2002-115093/16.  
DR N-PSDB; ABA93409.  
XX  
XX Human nuclear transcription factor-2 gene encoded protein, useful for treating related disease.  
XX  
XX Claim 1; Page 1 (Claims); 7pp; Chinese.  
XX  
XX The present sequence represents the human nuclear transcription factor-2, designated NFX2. The NFX2 gene has a cDNA sequence of 3613 base pairs (bp) containing an open reading frame sequence of 3075 bp from position 62 to 3136, encoding a sequence of 1024 amino acids and having a Genbank number of AF332009. The present invention also describes: (1) utilising the NFX2 gene to prepare a fusion protein; (2) utilising the protein to immunise an animal and to prepare monoclonal and polyclonal antibodies; and (3) utilising the gene in preparing testicular specific function gene expressing chips. The expressed protein may be useful in gene therapy for treating related disease. The NFX2 gene has been located to human chromosome 9

XX SQ Sequence 1024 AA;

Query Match 30.0%; Score 65; DB 5; Length 1024;  
Best Local Similarity 34.1%; Pred. No. 1.4e+02;  
Matches 15; Conservative 4; Mismatches 15; Indels 10; Gaps 3;

Qy 2 SCNGVCSPFEMPPCG-----TSACRC-----IPVGLVIG-YCRNP 35  
: ||||| ||||| : : : : :  
Db 456 SCNLLCHPGPCPCPFMTKTCGRTTRHTVRCQAVSVHCSPN 499

RESULT 9  
ADJ69675  
ID ADJ69675 standard; protein; 1024 AA.  
XX  
AC ADJ69675;  
XX  
DT 06-MAY-2004 (first entry)



[illegible]



Matches	12;	Conservative	4;	Mismatches	15;	Indels	2;	Gaps	1;
QY	7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37								
	:	:	:	:	:	:	:	:	:
Db	816 CAPGYGFGPTGCGACQCSPRGALSSLCERTSG 848								
	:	:	:	:	:	:	:	:	:
RESULT 15									
AAMS0360	ID AAMS0360 standard; protein; 1798 AA.								
XX									
AC	AAMS0360;								
XX									
XX	18-FEB-2002 (first entry)								
XX									
DE	Human laminin-15 beta 2 chain.								
XX									
KW	Laminin-15; human; retina; eye; therapy; ophthalmological;								
KW	antiinflammatory; rod dystrophy; rod-cone dystrophy;								
KW	retinitis pigmentosa; macular degeneration; retinal detachment.								
XX									
OS	Homo sapiens.								
XX									
PN	WO200183516-A1.								
XX									
PD	08-NOV-2001.								
XX									
PF	01-MAY-2001; 2001WO-US013943.								
XX									
PR	01-MAY-2000; 2000US-0200863P.								
XX									
PA	(MASS-) MASSACHUSETTS GEN HOSPITAL.								
XX									
PI	Burgeon RE, Brunken W, Champlaud M, Hunter D;								
XX									
DR	WPI; 2002-041478/05.								
DR	N-PSDB; AAI70819.								
XX									
PT	Novel substantially pure preparation comprising laminin having laminin								
PT	chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders								
PT	such as retinitis pigmentosa, macular degeneration, retinal detachment.								
XX									
PS	Disclosure; Fig 4A; 58pp; English.								
XX									
CC	The present sequence is that of the beta 2 chain of human laminin-15, a								
CC	novel member of the laminin family that is produced in the retina. The								
CC	retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2,								
CC	gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed								
CC	within the inter-photoreceptor matrix and in the outer plexiform layer,								
CC	and may serve to stabilise retinal synapses. The invention provides								
CC	laminin-15 preparations and cells comprising a nucleic acid encoding the								
CC	laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of								
CC	producing laminin-15. The laminin-15 preparation is used in claimed								
CC	methods of: increasing retina immunophoreceptor matrix stability;								
CC	increasing the stability of retina photoreceptor compounds, especially an								
CC	outer segment, inner segment or synapse; increasing retina adhesion;								
CC	treating a disorder associated with retina degeneration, especially rod								
CC	dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration								
CC	and retinal detachment; increasing the stability of synapses of the								
CC	central nervous system or peripheral nervous system; stimulating								
CC	neuroregeneration, axon outgrowth or synapse formation; preparing an								
CC	implant, e.g. a catheter, artificial joint, retinal implant, timed								
CC	releasing device, neural cell growth guide or artificial tissue, by								
CC	coating with the laminin-15 preparation; and increasing photosensitivity								
CC	by implanting a tip coated with the laminin-15 preparation into an eye.								
CC	The laminin may be recombinant, and the 3 chains co-expressed in the same								
CC	cell or expressed in different cells								
XX									
SQ	Sequence 1798 AA;								
Query Match	28.6%; Score 62; DB 5; Length 1798;								
Best Local Similarity	36.4%; Pred. No. 4.6e+02;								
Matches	12;	Conservative	4;	Mismatches	15;	Indels	2;	Gaps	1;

PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144353P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 28-JUL-1999; 99US-0145951P.  
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PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
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PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.

PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
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PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
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PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 28.1%; Score 61; DB 3; Length 94;  
Best Local Similarity 35.7%; Pred. NO. 45;  
Matches 15; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

Qy 7 CSPFEMPPCGT-----SACRCIVP-----GLVIGYCRNPS 36  
|||::|||  
Db 29 CSPMQLSPCATAITSSPFSALCCAKLKEQRPCLCGYMRNPS 70

RESULT 17







PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142803P.  
PR 08-JUL-1999; 99US-0142920P.  
PR 09-JUL-1999; 99US-0142977P.  
PR 12-JUL-1999; 99US-0143542P.  
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PR 16-JUL-1999; 99US-0144325P.  
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PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145226P.  
PR 27-JUL-1999; 99US-0145913P.  
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AC AAG37330;

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DT 18-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

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Query Match 27.9%; Score 60.5; DB 8; Length 681;  
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XX	XX		
KW	Cytostatic; Antinflammatory; Immunosuppressi		
KW	cancer; inflammatory; immune; human secreted		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO2004035732-A2.		
XX	XX		
PD	29-APR-2004.		
XX	XX		
PF	28-AUG-2003; 2003WO-US026780.		
XX	XX		
PR	29-AUG-2002; 2002US-0406576P.		
PR	29-AUG-2002; 2002US-0406579P.		
PR	29-AUG-2002; 2002US-0406585P.		
PR	29-AUG-2002; 2002US-0406588P.		
PR	29-AUG-2002; 2002US-0406608P.		
PR	29-AUG-2002; 2002US-0406611P.		
PR	29-AUG-2002; 2002US-0406612P.		
PR	29-AUG-2002; 2002US-0406616P.		
PR	29-AUG-2002; 2002US-0406640P.		
PR	29-AUG-2002; 2002US-0406642P.		
PR	29-AUG-2002; 2002US-0406646P.		
PR	29-AUG-2002; 2002US-0406653P.		
PR	29-AUG-2002; 2002US-0406655P.		
PR	29-AUG-2002; 2002US-0406666P.		
PR	17-SEP-2002; 2002US-0410946P.		
PR	17-SEP-2002; 2002US-0410947P.		
PR	17-SEP-2002; 2002US-0410948P.		
PR	17-SEP-2002; 2002US-0410949P.		
PR	17-SEP-2002; 2002US-0410953P.		
PR	17-SEP-2002; 2002US-0410957P.		
PR	17-SEP-2002; 2002US-0410958P.		
PR	17-SEP-2002; 2002US-0410959P.		
PR	17-SEP-2002; 2002US-0410960P.		
PR	17-SEP-2002; 2002US-0410961P.		
PR	17-SEP-2002; 2002US-0410962P.		
PR	17-SEP-2002; 2002US-0411019P.		
PR	17-SEP-2002; 2002US-0411022P.		
PR	17-SEP-2002; 2002US-0411023P.		
PR	17-SEP-2002; 2002US-0411024P.		
PR	17-SEP-2002; 2002US-0411032P.		
PR	17-SEP-2002; 2002US-0411035P.		
PR	17-SEP-2002; 2002US-0411037P.		
PR	17-SEP-2002; 2002US-0411041P.		
PR	17-SEP-2002; 2002US-0411045P.		
PR	17-SEP-2002; 2002US-0411046P.		
PR	17-SEP-2002; 2002US-0411048P.		
PR	17-SEP-2002; 2002US-0411052P.		
PR	17-SEP-2002; 2002US-0411055P.		
PR	17-SEP-2002; 2002US-0411073P.		
PR	17-SEP-2002; 2002US-0411082P.		
PR	17-SEP-2002; 2002US-0411101P.		
PR	17-SEP-2002; 2002US-0411111P.		
PR	18-APR-2003; 2003US-0463700P.		
PR	18-APR-2003; 2003US-0463708P.		
PR	18-APR-2003; 2003US-0463716P.		
PR	18-APR-2003; 2003US-0463732P.		

Query Match 27.9%; Score 60.5; DB 8; Length 681;





XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Hallenbeck RF, Huang WM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
DR  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
XX Claim 1; SEQ ID NO 1282; 428pp; English.  
XX  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC anti-inflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
XX Sequence 576 AA;  
SQ  
Query Match 27.4%; Score 59.5; DB 8; Length 576;  
Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
Matches 12; Conservative 2; Mismatches 9; Indels 1; Gaps 1;  
QY 15 CGTSACR-CIPVGLVIGYCRNPSG 37  
Db 108 CGIKSCRGLDQGLDDNYCRNPDG 131  
Search completed: March 28, 2005, 08:57:08  
Job time : 97 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:40:49 ; Search time 84 Seconds  
(without alignments)  
225.559 Million cell updates/sec

Title: US-09-674-496d-8

Perfect score: 222

Sequence: 1 ADCNGACSPPEVPCRSRDCRCPDGLVFGFCIHPTG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	222	100.0	119	1	ALB1_SOYBN	Q9837 glycine max
2	216	97.3	119	1	ALB1_GLYSO	Q92x0 glycine soj
3	208	93.7	100	2	Q7XZC3	Q7xzc3 glycine max
4	192	86.5	89	1	ALB1_PHAU	Q9frt8 phaseolus a
5	169	76.1	96	2	O6A1C7	O6alc7 vicia hirsu
6	168	75.7	140	2	Q7XZC5	Q7xzc5 medicago tr
7	165	74.3	130	1	AL1B_PEA	P62927 pisum sativ
8	163	73.4	100	2	O6A1D7	O6ald7 astragalus
9	161.5	72.7	90	1	ALB1_PHAAN	Q9frt9 phaseolus a
10	161	72.5	91	2	O6A1D6	O6ald6 alysicarpus
11	161	72.5	130	1	AL1D_PEA	P62929 pisum sativ
12	158	71.2	98	2	O6A1C9	O6alc9 onobrychis
13	158	71.2	130	1	AL1E_PEA	P62930 pisum sativ
14	155	69.8	130	1	AL1A_PEA	P62926 pisum sativ
15	154	69.4	99	2	O6A1C8	O6alc8 trigonella
16	154	69.4	130	1	AL1F_PEA	P62931 pisum sativ
17	152	68.5	98	2	O6A1D4	O6ald4 canavalia b
18	151	68.0	99	2	O6A1D5	O6ald5 bituminaria
19	148.5	66.9	109	2	Q7XZC2	Q7xzc2 phaseolus v
20	137.5	61.9	101	2	O6A1D3	O6ald3 lonchocarpu
21	136	61.3	130	1	AL1C_PEA	P62928 pisum sativ
22	128	57.7	98	2	O6A1D2	O6ald2 melilotus a
23	125	56.3	81	1	ALB1_LUPAN	Q96474 lupinus ang
24	124.5	56.1	101	2	O6A1D1	O6ald1 mundulea se
25	121	54.5	142	2	Q7XZC4	Q7xzc4 medicago tr
26	109	49.1	58	2	O6A1B9	O6alb9 vigna ungui
27	109	49.1	58	2	O6A1C0	O6alc0 vigna subte
28	103	46.4	59	2	O6A1C3	O6alc3 lathyrus la
29	99.5	44.8	101	2	O6A1D0	O6ald0 mundulea se
30	88	39.6	60	2	O6A1C2	O6alc2 mundulea se
31	83	37.4	58	2	O6A1C4	O6alc4 canavalia b

32	83	37.4	59	2	O6A1C6	Q6alc6 bituminaria
33	80	36.0	60	2	O6A1C1	Q6alc1 onobrychis
34	72	32.4	58	2	O6A1C5	Q6alc5 caragana ar
35	69	31.1	370	2	Q7Q894	Q7q894 giardia lam
36	64	28.8	536	2	Q8IHD9	Q8ihd9 drosophila
37	64	28.8	539	2	O8MLS4	O8mls4 drosophila
38	63	28.4	3075	1	LMAL_HUMAN	P25391 homo sapien
39	62.5	28.2	379	1	WIFI_HUMAN	Q935W5 homo sapien
40	62.5	28.2	379	2	O6UX11	O6ux11 homo sapien
41	61.5	27.7	1847	2	O76952	O76952 aedes aegyp
42	60.5	27.3	220	2	O99KR2	O99kr2 mus musculu
43	60.5	27.3	365	2	Q924V6	Q924v6 rattus norv
44	60.5	27.3	379	1	WIFI_MOUSE	Q9xual mus musculu
45	60.5	27.3	379	2	O6IN38	O6in38 rattus norv
46	59	26.6	3084	1	LMAL_MOUSE	P19137 mus musculu
47	58.5	26.4	592	2	O7QT99	Q7qt99 giardia lam
48	58	26.1	494	2	O6DJ29	O6dj29 xenopus tro
49	57.5	25.9	87	1	OM3_CHLPS	P27606 chlamydia p
50	57.5	25.9	421	2	O7PS97	O7ps97 anopheles g
51	57.5	25.9	440	2	P90769	P90769 caenorhabdi
52	57.5	25.9	574	2	O7R5J3	Q7r5j3 giardia lam
53	57.5	25.9	618	2	O69ZA9	O69za9 mus musculu
54	57.5	25.9	3550	2	O66GT4	O66gt4 rattus norv
55	57.5	25.9	7524	2	O6P2E0	O6p2e0 mus musculu
56	57	25.7	88	2	P94663	P94663 chlamydophi
57	57	25.7	91	2	O8H0Y6	O8h0y6 arabidopsis
58	57	25.7	92	2	O8L7G7	O8l7g7 arabidopsis
59	57	25.7	636	2	O942D3	O942d3 oryza sativ
60	57	25.7	722	1	SOA1_HUMAN	Q96bd0 h solute ca
61	56.5	25.5	87	2	O9A1S8	O9a1s8 chlamydophi
62	56.5	25.5	371	2	O72BJ2	Q72bj2 desulfovibr
63	56	25.2	324	1	IBP2_CHICK	P49705 gallus gall
64	56	25.2	324	2	O7RAW1	O7raw1 plasmodium
65	56	25.2	404	2	O61FW1	O61fw1 rattus norv
66	55.5	25.0	175	2	O9PZK6	O9pzk6 human cytom
67	55.5	25.0	389	2	O97887	O97887 bos taurus
68	55.5	25.0	461	1	PRTC_RAT	P21394 rattus norv
69	55.5	25.0	514	2	O6INT8	O6int8 xenopus lae
70	55.5	25.0	717	2	O8AXR0	O8axr0 xenopus lae
71	55.5	25.0	1637	2	O9XSV8	O9xsv8 bos taurus
72	55.5	25.0	5146	2	O8SPM4	O8spm4 bos taurus
73	55	24.8	200	2	O86YU6	O86yu6 homo sapien
74	55	24.8	284	2	O66T09	O66t09 brachydanio
75	55	24.8	274	2	O6W4T8	O6w4t8 brachydanio
76	55	24.8	820	2	O9FFK8	Q9ffk8 arabidopsis
77	54.5	24.5	85	1	CVPI_PIMHY	Q8t0w5 pimpla hypo
78	54.5	24.5	123	1	D126_MACFA	O8bee3 macaca fasc
79	54.5	24.5	131	2	O9NB50	Q9nb50 riftia pach
80	54.5	24.5	921	2	O6CF14	O6cf14 kluyveromyc
81	54.5	24.5	965	1	YNC3_YEAST	P53971 saccharomyc
82	54	24.3	61	1	MT1A_BOVIN	P67983 bos taurus
83	54	24.3	61	1	MT1A_SHEEP	P67982 ovis aries
84	54	24.3	61	1	MT1B_SHEEP	P09577 ovis aries
85	54	24.3	61	1	MT1C_SHEEP	P09578 ovis aries
86	54	24.3	61	2	O8MI14	Q8mi14 bos taurus
87	54	24.3	61	2	O6R522	O6r522 bos mutus g
88	54	24.3	819	2	O672W0	Q672w0 aspergillus
89	54	24.3	1299	2	O8MQ37	Q8mq37 caenorhabdi
90	54	24.3	1587	2	LMG3_HUMAN	O9y6n6 homo sapien
91	54	24.3	2427	2	O8MQ36	O8mq36 caenorhabdi
92	53.5	24.1	110	2	O67WJ9	Q67wj9 oryza sativ
93	53.5	24.1	277	2	O9XZ11	O9xz11 leishmania
94	53.5	24.1	371	2	O18285	O18285 caenorhabdi
95	53.5	24.1	374	1	WIFI_XENLA	Q9w6f8 xenopus lae
96	53.5	24.1	1859	2	O7PS28	Q7ps28 anopheles g
97	53.5	24.1	2585	2	O23587	O23587 caenorhabdi
98	53	23.9	61	1	MT1_BOVIN	P58280 bos taurus
99	53	23.9	119	2	O9CVT5	O9cvt5 mus musculu
100	53	23.9	140	2	O49628	O49628 arabidopsis

ALIGNMENTS

```

RESULT 1
ALB1_SOYBN STANDARD; PRT; 119 AA.
ID Q39837; Q49854;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 precursor (Al1) [Contains: Albumin 1 chain b (Alb)
  (Legnulin); Albumin 1 chain a (Ala)].
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagishiroe; TISSUE=Radicle;
RX MEDLINE=94357216; PubMed=8076638;
RA Watanabe Y., Barbaehov S.F., Komatsu S., Hemmings A.M., Miyagi M.,
RA Teunasaawa S., Hirano H.;
RT "A peptide that stimulates phosphorylation of the plant insulin-
RT binding protein. Isolation, primary structure and cDNA cloning.";
RL Eur. J. Biochem. 224:167-172(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagishiroe;
RA Tan J.Z., Lou C.F., Hirano H.;
RT "Analysis of legumin gene in soybean cultivar (Glycine max) and
RT wild species (Glycine soja).";
RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).
RN [3]
RP REVISION TO 64.
RC STRAIN=cv. Miyagishiroe;
RA Hirano H.;
RT Submitted (JUN-2001) to Swiss-Prot.
RN [4]
RP STRUCTURE BY NMR OF 20-56, MUTAGENESIS OF ARG-35; VAL-48 AND PHE-50,
RP AND FUNCTION.
RX PubMed=12631285;
RA Yamazaki T., Takaoka M., Kato E., Hanada K., Sakita M., Sakata K.,
RA Nishuchi Y., Hirano H.;
RT "A possible physiological function and the tertiary structure of a 4-
RT kDa peptide in legumes.";
RL Eur. J. Biochem. 270:1269-1276(2003).
CC -!- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide.
CC -!- PTM: The C-terminal glycine may be removed from Alb.
CC -----
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CC -----
DR EMBL; D17396; BAA04219.1; -.
DR EMBL; AJ223037; CAA11040.1; -.
DR F01; S48192; S48192.
DR PDB; 1J08; NMR; A=20-56.
KW 3D-structure; Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 56 Albumin 1 chain b.
FT PROPEP 57 64 Potential.
FT CHAIN 65 116 Albumin 1 chain a (Potential).
FT PROPEP 117 119 Potential.
FT DISULFID 22 39 By similarity.
FT DISULFID 26 41 By similarity.
FT DISULFID 34 51 By similarity.
SQ SEQUENCE 119 AA; 12963 MW; EE5457D8D09070CC CRC64;
Query Match 97.3%; Score 216; DB 1; Length 119;
Best Local Similarity 97.3%; Pred. No. 1.3e-19;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
Q7XZC3 PRELIMINARY; PRT; 100 AA.
ID Q7XZC3
AC Q7XZC3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Albumin 1 precursor (Fragment).  
 GN Name=pal;  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;  
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OC NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,  
 RA Vallier A., Rabbe Y.;  
 RT "Molecular and biological screening for insect-toxic seed albumins  
 RT from four legume species.";  
 RL Plant Sci. 167:705-714(2004).  
 DR EMBL; AJ574791; CAB00463.1; -.  
 DR HSSP; Q39837; IJ08.  
 KW Signal.  
 FT SIGNAL. 1 19 Potential.  
 FT CHAIN 20 56 Alb, albumin 1b.  
 FT CHAIN 65 >100 Ala, albumin 1a.  
 FT NON TER 100 100  
 SQ SEQUENCE 100 AA; 10982 MW; 281D9CE0F8B83611 CRC64;  
 Query Match 93.7%; Score 208; DB 2; Length 100;  
 Best Local Similarity 91.9%; Pred. No. 1.1e-18;  
 Matches 34; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ADCNGACSPPEVPPCRSRDCRCVPGLGVGFCIHPTG 37  
 Db 20 ADCNGACSPPEVPPCRSRDCRCVPGLGVGFCIHPTG 56  
 RESULT 4  
 ALB1\_PHAU  
 ID ALB1\_PHAU STANDARD; PRT; 89 AA.  
 AC Q9FRT8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Albumin 1 precursor (Al) [Contains: Albumin 1 chain b (Alb)  
 DE (Leguminin); Albumin 1 chain a (Ala)] (Fragment).  
 GN Name=LEG;  
 OS Phaseolus aureus (Mung bean) (Vigna radiata).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;  
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
 OC NCBI\_TaxID=3916;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=cv. Blackmappe; TISSUE=Leaf;  
 RX PubMed=12631285;  
 RA Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K.,  
 RA Nishitani Y., Hirano H.;  
 RT "A possible physiological function and the tertiary structure of a 4-  
 RT kDa peptide in legumes.";  
 RL Eur. J. Biochem. 270:1269-1276(2003).  
 CC -1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its  
 CC phosphorylation activity (By similarity).  
 CC -1- PTM: The C-terminal glycine may be removed from Alb.  
 CC -----  
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 CC -----  
 DR EMBL; AB052881; BAB19938.1; -.  
 DR HSSP; Q39837; IJ08.  
 KW Plant toxin; Seed storage protein; Signal.

FT NON TER 1 1 Potential.  
 FT SIGNAL <1 1 Albumin 1 chain b (By similarity).  
 FT CHAIN 38 38 Albumin 1 chain a (Potential).  
 FT PROPEP 39 46  
 FT CHAIN 47 >89 Albumin 1 chain a (Potential).  
 FT DISULFID 4 21 By similarity.  
 FT DISULFID 8 23 By similarity.  
 FT DISULFID 16 33 By similarity.  
 FT NON TER 89 89  
 SQ SEQUENCE 89 AA; 9711 MW; 4ADEB9797083135B CRC64;  
 Query Match 86.5%; Score 192; DB 1; Length 89;  
 Best Local Similarity 83.8%; Pred. No. 1.1e-16;  
 Matches 31; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ADCNGACSPPEVPPCRSRDCRCVPGLGVGFCIHPTG 37  
 Db 2 ADCNGACSPPEVPPCRSRDCRCVPGLGVGFCIHPTG 38  
 RESULT 5  
 Q6A1C7  
 ID Q6A1C7 PRELIMINARY; PRT; 96 AA.  
 AC Q6A1C7;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Putative albumin 1 precursor (Fragment).  
 GN Name=pal;  
 OS Vicia hirsuta.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;  
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Vicia.  
 OC NCBI\_TaxID=3910;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
 RT "Gene structure, protein structure, and regulation of the synthesis of  
 RT a sulfur-rich protein in pea seeds.";  
 RL J. Biol. Chem. 261:11124-11130(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Dupont G., Diol.O.,  
 RA Chesel D., Rabbe Y.;  
 RT "Broad screening of the legume family for variability of insecticidal  
 RT activities and occurrence of seed albumin 1b toxins.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ784951; CAH05251.1; -.  
 KW Signal.  
 FT SIGNAL. 1 26 Potential.  
 FT CHAIN 27 63 putative albumin 1b.  
 FT CHAIN 69 >96 putative albumin 1a.  
 FT NON TER 96 96  
 SQ SEQUENCE 96 AA; 10546 MW; DD8EF1B021A73DD7 CRC64;  
 Query Match 76.1%; Score 169; DB 2; Length 96;  
 Best Local Similarity 67.6%; Pred. No. 9.3e-14;  
 Matches 25; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ADCNGACSPPEVPPCRSRDCRCVPGLGVGFCIHPTG 37  
 Db 27 AECNGVCSPPPEVPPCRSRDCRCVPGLGVGFCIHPTG 63  
 RESULT 6.  
 Q7XZC5  
 ID Q7XZC5 PRELIMINARY; PRT; 140 AA.  
 AC Q7XZC5;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Albumin 1 precursor.

GN Name=pai;  
 OS Medicago truncatula (Barrel medic).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.  
 OX NCBI\_TaxID=3880;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,  
 RA Vallier A., Rahbe Y.;  
 RT "Molecular and biological screening for insect-toxic seed albumins  
 RT from four legume species.";  
 RL Plant Sci. 167:705-714(2004).  
 DR EMBL; AJ574789; CAB00461.1; -.  
 DR HSSP; Q39837; 1JUB.  
 KW Signal.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 140 albumin 1.  
 SQ SEQUENCE 140 AA; 15426 MW; 519D9CEAB8924855 CRC64;  
 Query Match 75.7%; Score 168; DB 2; Length 140;  
 Best Local Similarity 71.4%; Pred. No. 1.8e-13;  
 Matches 25; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 DCGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPT 36  
 Db ||:|||||:|||||:|||||:|||||:|:|:|:  
 29 DCSGACSPFEMPCCRSDDCRICIGLVAGYCTYPS 63  
 RESULT 7  
 ALIB\_PEA STANDARD; PRT; 130 AA.  
 ID ALIB\_PEA  
 AC P6297; P08687; Q40999; Q9M3X4;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DE 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Albumin 1 B precursor (PA1 B) [Contains: Albumin 1 B chain b (PA1B B)  
 DE (Leginsulin B); Albumin 1 B chain a (PALA B)].  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
 OX NCBI\_TaxID=3888;  
 [1]  
 RN SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.  
 RC STRAIN=cv. Greenfeast; TISSUE=Seed;  
 RX MEDLINE=86278210; PubMed=3755437;  
 RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
 RT "Gene structure, protein structure, and regulation of the synthesis of  
 RT a sulfur-rich protein in pea seeds.";  
 RL J. Biol. Chem. 261:11124-11130(1986).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=cv. Birte; TISSUE=Cotyledon;  
 RC Domoney C., Ellis N., Welham T.;  
 RA "Genetic loci controlling albumin synthesis in Pisum.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PA1b binds to basic 7S globulin (BG) and stimulates its  
 CC phosphorylation activity. Involved in the signal transduction  
 CC system to regulate the growth and differentiation as a hormone  
 CC peptide. Toxic to various insects through binding to a high  
 CC affinity binding site in the insect gut (by similarity).  
 CC -!- TISSUE SPECIFICITY: Major component of both the cotyledons and  
 CC embryonic axes of mature seeds.  
 CC -!- DEVELOPMENTAL STAGE: Increasing expression during seed development  
 CC followed by a rapid degradation during the first days of seed  
 CC germination.  
 CC -!- PTM: The C-terminal glycine may be removed from PA1b.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M13790; AAA33639.1; -.  
 DR EMBL; AJ276882; CAB82859.1; -.  
 DR InterPro; IPR011036; PH related.  
 KW Plant toxin; Seed storage protein; Signal.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 63 Albumin 1 B chain b.  
 FT PROPEP 64 69 Potential.  
 FT CHAIN 70 122 Albumin 1 B chain a.  
 FT PROPEP 123 130 Potential.  
 FT DISULFID 29 46 By similarity.  
 FT DISULFID 33 48 By similarity.  
 FT DISULFID 41 58 By similarity.  
 FT CONFLICT 10 10 M -> I (in Ref. 2).  
 FT CONFLICT 120 120 Q -> P (in Ref. 2).  
 SQ SEQUENCE 130 AA; 13970 MW; F8B134A334490F5F CRC64;  
 Query Match 74.3%; Score 165; DB 1; Length 130;  
 Best Local Similarity 67.6%; Pred. No. 3.9e-13;  
 Matches 25; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37  
 Db |||:|||||:|||||:|||||:|||||:|:|:|:  
 27 ASCNGVCSPPFEMPCCGSACRCIPVLGVGYCRHPSG 63  
 RESULT 8  
 Q6A1D7 PRELIMINARY; PRT; 100 AA.  
 ID Q6A1D7  
 AC Q6A1D7;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Putative albumin 1 precursor (Fragment).  
 GN Name=pai;  
 OS Astragalus monspesulanus.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Galegeae; Astragalus.  
 OX NCBI\_TaxID=287756;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
 RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
 RT "Gene structure, protein structure, and regulation of the synthesis of  
 RT a sulfur-rich protein in pea seeds.";  
 RL J. Biol. Chem. 261:11124-11130(1986).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP Louis S., Delobel B., Gressent F., Rahioui I., Dupont G., Diol O.,  
 RA Chessel D., Rahbe Y.;  
 RT "Broad screening of the legume family for variability of insecticidal  
 RT activities and occurrence of seed albumin 1b toxins.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ784941; CAH05241.1; -.  
 KW Signal.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 64 putative albumin 1b.  
 FT CHAIN 73 >100 putative albumin 1a.  
 FT NON\_TER 100 100  
 SQ SEQUENCE 100 AA; 10941 MW; 7CE8C76BD196587A CRC64;  
 Query Match 73.4%; Score 163; DB 2; Length 100;  
 Best Local Similarity 72.2%; Pred. No. 5.6e-13;  
 Matches 26; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 DCGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37  
 Db ||:|||||:|||||:|||||:|||||:|:|:|:  
 29 DCSGACSPFEMPCCGSDDCRICIPWGLFVGECYPTG 64

```
RESULT 9
ALBI PHAAN STANDARD; PRT; 90 AA.
AC Q9FRT9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 precursor (Al) [Contains: Albumin 1 chain b (Alb)
DE (Leguminsulin); Albumin 1 chain a (Ala)] (Fragment).
GN NamesLEG;
OS Phaseolus angularis (Adzuki bean) (Vigna angularis).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OC NCBI_TaxID=3914;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Dainagonazuki; TISSUE=Leaf;
RX PubMed=12631285;
RA Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K.,
RA Nishitani Y., Hirano H.;
RT "A possible physiological function and the tertiary structure of a 4-
RT kDa peptide in legumes.";
RL Eur. J. Biochem. 270:1269-1276(2003).
CC -1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity (By similarity).
CC -1- PTM: The C-terminal glycine may be removed from Alb.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB052880; BAB19937.1; -.
DR HSSP; Q39837; 1JU8.
KW Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1 1 Potential.
FT CHAIN <1 1 Albumin 1 chain b (By similarity).
FT PROPEP 40 47 Potential.
FT CHAIN 48 >90 Albumin 1 chain a (Potential).
FT DISULFID 4 21 By similarity.
FT DISULFID 8 23 By similarity.
FT DISULFID 16 34 By similarity.
FT NON TER 90 90
SQ SEQUENCE 90 AA; 9701 MW; 070A562F346FB61 CRC64;

Query Match 72.7%; Score 161.5; DB 1; Length 90;
Best Local Similarity 68.4%; Pred. No. 7.8e-13;
Matches 26; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 ADCNGACSPFVPPCRSRDCRCVPIGLFVGFCIHPTG 37
Db 2 ADCNGACSPFQMPQCGSTDCICIPAGLLFVGICYTPSG 39

RESULT 10
Q6A1D6 PRELIMINARY; PRT; 91 AA.
AC Q6A1D6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative albumin 1 precursor (Fragment).
GN Namespal;
OS Alysicarpus ovalifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Query Match 72.5%; Score 161; DB 2; Length 91;
Best Local Similarity 73.0%; Pred. No. 9.1e-13;
Matches 27; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 ADCNGACSPFVPPCRSRDCRCVPIGLFVGFCIHPTG 37
Db 19 ADCSGACSPFRLPGSTDCRCIPVLLAGFCIYPTG 55

RESULT 11
ALLD_PEA STANDARD; PRT; 130 AA.
AC P62929; P08687; Q40999; Q7XK6; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 D precursor (PA1 D) (PsaAlb012) [Contains: Albumin 1 D chain
DE b (Palb D) (Leginsulin D); Albumin 1 D chain a (Pala D)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OC NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Frisson; TISSUE=Seed;
RA Louis S., Delobel B., Gressent F., Rahoui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
RN [2]
RP SEQUENCE OF 70-122, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide. Toxic to various insects through binding to a high
CC affinity binding site in the insect gut (By similarity).
CC -1- TISSUE SPECIFICITY: Major component of both the cotyledons and
CC embryonic axes of mature seeds.
CC -1- DEVELOPMENTAL STAGE: Increasing expression during seed development
```

CC followed by a rapid degradation during the first days of seed  
 CC germination.  
 CC -1- PPM: The C-terminal glycine may be removed from PALb.  
 CC -1- MISCELLANEOUS: The protein sequenced in Ref.2 was probably a  
 CC mixture of the products of genes C and D, PALb being of C origin  
 CC while Pala is of D origin.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AJ574794; CAB00466.1; --  
 CC InterPro: IPR011036; PH related.  
 CC Direct protein sequencing; Plant toxin; Seed storage protein; Signal.  
 KW SIGNAL 1 26 Potential.  
 FT CHAIN 27 63 Albumin 1 D chain b.  
 FT PROPEP 64 69  
 FT CHAIN 70 122 Albumin 1 D chain a.  
 FT PROPEP 123 130  
 FT DISULFID 29 46 By similarity.  
 FT DISULFID 33 48 By similarity.  
 FT DISULFID 41 58 By similarity.  
 SQ SEQUENCE 130 AA; 13916 MW; 823AA340ACD9535C CRC64;  
 Query Match 72.5%; Score 161; DB 1; Length 130;  
 Best Local Similarity 62.2%; Pred. No. 1.3e-12;  
 Matches 23; Conservative 8; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ADCNGACSPFEPVPCRSRDCRCVPIGLFVGFCIHPTG 37  
 Db 27 ASCNGCVSPFEMPFCGTSACRCIPVGLFVFCYCRNPSG 63  
 RESULT 12  
 Q6A1C9 PRELIMINARY; PRT; 98 AA.  
 AC Q6A1C9  
 DT 25-OCT-2004 (TEMBUREL. 28, Created)  
 DT 25-OCT-2004 (TEMBUREL. 28, Last sequence update)  
 DT 25-OCT-2004 (TEMBUREL. 28, Last annotation update)  
 DE Putative albumin 1 precursor (Fragment).  
 GN Name=pal;  
 OS Onobrychis vicifolia (Common sainfoin).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Hedyseae; Onobrychis.  
 OX NCBI\_TaxID=3882;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
 RA "Glenn R.J., Kortt A.A., Inglis A.S.;  
 RT "Blaug structure, protein structure, and regulation of the synthesis of  
 RT a sulfur-rich protein in pea seeds.";  
 RL J. Biol. Chem. 261:11124-11130(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Dupont G., Diol O.,  
 RA Chesnel D., Rahbe Y.;  
 RT "Broad screening of the legume family for variability of insecticidal  
 RT activities and occurrence of seed albumin lb toxins.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ784949; CAH05249.1; --  
 KW SIGNAL 1 28 Potential.  
 FT CHAIN 29 63 putative albumin lb.  
 FT CHAIN 71 >98 putative albumin la.  
 FT NON TER 98 98  
 SQ SEQUENCE 98 AA; 10830 MW; 03072C77178A1E83 CRC64;

Query Match 71.2%; Score 158; DB 2; Length 98;  
 Best Local Similarity 76.5%; Pred. No. 2.3e-12;  
 Matches 26; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 CNGACSPFEPVPCRSRDCRCVPIGLFVGFCIHPT 36  
 Db 29 CDGVCSPFEMPFCGSDCRCVPMGLFVGQCINPT 62  
 RESULT 13  
 ALIE\_PEA STANDARD; PRT; 130 AA.  
 ID ALIE\_PEA  
 AC PE2930; P08687; Q40999; Q7XZC1; Q9M3X4;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Albumin 1 E precursor (PAL E) (PsaAlb014) (Psa) [Contains: Albumin 1 E  
 DE chain b (PALb E) (leguminsulin E); Albumin 1 E chain a (PALa E)].  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Greenfeast;  
 RX PubMed=9749674;  
 RA Morton R.L., Ellery A.J., Higgins T.J.;  
 RT "Downstream elements from the pea albumin 1 gene confer sulfur  
 RT responsiveness on a reporter gene.";  
 RL Mol. Gen. Genet. 259:309-316(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Frisson; TISSUE=Seed;  
 RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,  
 RA Vallier A., Rahbe Y.;  
 RT "Molecular and biological screening for insect-toxic seed albumins  
 RT from four legume species.";  
 RL Plant Sci. 167:705-714(2004).  
 CC -1- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its  
 CC phosphorylation activity. Involved in the signal transduction  
 CC system to regulate the growth and differentiation as a hormone  
 CC peptide. Toxic to various insects through binding to a high  
 CC affinity binding site in the insect gut (By similarity).  
 CC -1- PTM: The C-terminal glycine may be removed from PALb.  
 CC -----  
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 CC -----  
 CC EMBL: M81864; AAC61879.1; --  
 CC EMBL: AJ574795; CAE00467.1; --  
 CC InterPro: IPR011036; PH related.  
 KW Plant toxin; Seed storage protein; Signal.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 63 Albumin 1 E chain b.  
 FT PROPEP 64 69 Potential.  
 FT CHAIN 70 122 Albumin 1 E chain a.  
 FT PROPEP 123 130 Potential.  
 FT DISULFID 29 46 By similarity.  
 FT DISULFID 33 48 By similarity.  
 FT DISULFID 41 58 By similarity.  
 SQ SEQUENCE 130 AA; 13778 MW; C534DE67A304F749 CRC64;  
 Query Match 71.2%; Score 158; DB 1; Length 130;  
 Best Local Similarity 62.2%; Pred. No. 3e-12;  
 Matches 23; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ADCNGACSPFEPVPCRSRDCRCVPIGLFVGFCIHPTG 37





RA Jouvansal L., Quillien L., Ferrasson E., Rahbe Y., Gueguen J.,  
RA Vovelle F.;  
RT "PALB, an insecticidal protein extracted from pea seeds (*Pisum*  
RT sativum): 1H-2-D NMR study and molecular modeling.";  
RL Biochemistry 42:11915-11923(2003).  
RN [4]  
RP FUNCTION.  
RX PubMed=12755698;  
RA Gressent F., Rahiou I., Rahbe Y.;  
RT "Characterization of a high-affinity binding site for the pea albumin  
RT lb entomotoxin in the weevil *Sitophilus*.";  
RL Eur. J. Biochem. 270:2429-2435(2003).  
CC -1- FUNCTION: PALB binds to basic 7S globulin (BG) and stimulates its  
CC phosphorylation activity. Involved in the signal transduction  
CC system to regulate the growth and differentiation as a hormone  
CC peptide (by similarity). Toxic to various insects through binding  
CC to a high affinity binding site in the insect gut.  
CC -1- PTM: The C-terminal glycine may be removed from PALB.  
CC -1- PTM: PALB displays a cysteine-knot (knottin) fold.  
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CC -----  
DR EMBL; AJ574793; CAE00465.1; -.  
DR PDB; 1P8B; NMR; A=27-63.  
DR InterPro; IPR011036; Pfam related.  
DR 3D-structure; Direct protein sequencing; Plant toxin;  
KW Seed storage protein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 63 Albumin 1 F chain b.  
FT PROPEP 64 69 Potential.  
FT CHAIN 70 122 Albumin 1 F chain a.  
FT PROPEP 123 130 Potential.  
FT DISULFID 29 46  
FT DISULFID 33 48  
FT DISULFID 41 58  
SQ SEQUENCE 130 AA; 13913 MW; FDS8E2D3C99D1644 CRC64;  
  
Query Match 69.4%; Score 154; DB 1; Length 130;  
Best Local Similarity 59.5%; Pred. No. 9.7e-12;  
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 A D C G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 37  
DB 27 A S C N G V C S P F E M P P C G T S A C R C I P V G L V I G Y C R N P S G 63  
  
RESULT 17  
Q6ALD4  
ID Q6ALD4 PRELIMINARY; PRT; 98 AA.  
AC Q6ALD4  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Putative albumin 1 precursor (Fragment).  
GN Name=pal;  
OS Canavalia brasiliensis (Brazilian jack bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Canavalia.  
OX NCBI\_TaxID=61861;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
RT "Gene structure, protein structure, and regulation of the synthesis of  
RT a sulfur-rich protein in pea seeds";  
RL J. Biol. Chem. 261:11124-11130(1986).  
  
SEQUENCE FROM N.A.  
Louis S., Delobel B., Gressent F., Rahiou I., Duport G., Diol O.,  
Chessel D., Rahbe Y.;  
RT "Broad screening of the legume family for variability of insecticidal  
RT activities and occurrence of seed albumin lb toxins.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784943; CAH05243.1; -.  
KW Signal.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 62 putative albumin lb.  
FT CHAIN 72 >99 putative albumin la.  
FT NON\_TER 99 99  
SQ SEQUENCE 99 AA; 10767 MW; 27ACD82ABC4B2B92 CRC64;  
  
Query Match 68.0%; Score 151; DB 2; Length 99;  
Best Local Similarity 71.4%; Pred. No. 1.8e-11;  
Matches 25; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
QY 3 C N G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 37  
DB 28 C S G A C F P F Q M P P C G S T D C R C V P W G L F V G Q C I D P I G 62  
  
RESULT 19  
Q7XZC2  
ID Q7XZC2 PRELIMINARY; PRT; 109 AA.

RN SEQUENCE FROM N.A.  
RA Louis S., Delobel B., Gressent F., Rahiou I., Duport G., Diol O.,  
RA Chessel D., Rahbe Y.;  
RT "Broad screening of the legume family for variability of insecticidal  
RT activities and occurrence of seed albumin lb toxins.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784944; CAH05244.1; -.  
KW Signal.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 62 putative albumin lb.  
FT CHAIN 71 >98 putative albumin la.  
FT NON\_TER 98 98  
SQ SEQUENCE 98 AA; 10484 MW; B28B2E3919403D53 CRC64;  
  
Query Match 68.5%; Score 152; DB 2; Length 98;  
Best Local Similarity 67.6%; Pred. No. 1.3e-11;  
Matches 23; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
  
QY 3 C N G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 36  
DB 28 C S G G C S P F E M P P C G S D C R C I P W G L V A G Y C I N P T 61  
  
RESULT 18  
Q6ALD5  
ID Q6ALD5 PRELIMINARY; PRT; 99 AA.  
AC Q6ALD5  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Putative albumin 1 precursor (Fragment).  
GN Name=pal;  
OS Bituminaria bituminosa.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Psoraleae;  
OC Bituminaria.  
OX NCBI\_TaxID=53836;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,  
RA Blagrove R.J., Kortt A.A., Inglis A.S.;  
RT "Gene structure, protein structure, and regulation of the synthesis of  
RT a sulfur-rich protein in pea seeds";  
RL J. Biol. Chem. 261:11124-11130(1986).  
  
SEQUENCE FROM N.A.  
Louis S., Delobel B., Gressent F., Rahiou I., Duport G., Diol O.,  
Chessel D., Rahbe Y.;  
RT "Broad screening of the legume family for variability of insecticidal  
RT activities and occurrence of seed albumin lb toxins.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784943; CAH05243.1; -.  
KW Signal.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 62 putative albumin lb.  
FT CHAIN 72 >99 putative albumin la.  
FT NON\_TER 99 99  
SQ SEQUENCE 99 AA; 10767 MW; 27ACD82ABC4B2B92 CRC64;  
  
Query Match 68.0%; Score 151; DB 2; Length 99;  
Best Local Similarity 71.4%; Pred. No. 1.8e-11;  
Matches 25; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
QY 3 C N G A C S P F E V P P C R S R D C R C V P I G L F V G F C I H P T G 37  
DB 28 C S G A C F P F Q M P P C G S T D C R C V P W G L F V G Q C I D P I G 62  
  
RESULT 19  
Q7XZC2  
ID Q7XZC2 PRELIMINARY; PRT; 109 AA.

```

AC Q7XZC3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Albumin 1 precursor (Fragment).
GN Names=pal;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
DR EMBL; AJ574792; CAE00464.1; -.
DR HSSP; Q39837; 1J08.
KW Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 65 Alb, albumin 1b.
FT CHAIN 74 >109 Ala, albumin 1a.
FT NON TER 109 109
FT SEQUENCE 109 AA; 11923 MW; E420417E90D351AE CRC64;

Query Match 66.9%; Score 148.5; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 4.1e-11;
Matches 24; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 3 CNGACSPFPPPCRS-RDRCVPIGLFVGFCIHPTG 37
DB 30 CSGVCSPFPPPCGSTRDRCVPIGLFVGFCIHTYPSG 65

RESULT 20
Q6ALD3 ID Q6ALD3 PRELIMINARY; PRT; 101 AA.
AC Q6ALD3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative albumin 1 precursor (Fragment).
GN Names=pal;
OS Lonchocarpus capassa (Apple-leaf).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Millettieae;
OC Lonchocarpus.
OX NCBI_TaxID=3926;
RN [1]
RP SEQUENCE FROM N.A.
RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
RA Chesnel D., Rahbe Y.;
RT "Broad screening of the legume family for variability of insecticidal
RT activities and occurrence of seed albumin 1b toxins.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784945; CAH05245.1; -.
KW Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 65 putative albumin 1b.
FT CHAIN 74 >101 putative albumin 1a.
FT NON TER 101 101
FT SEQUENCE 101 AA; 11003 MW; 0B8A138465E7C19B CRC64;

Query Match 61.9%; Score 137.5; DB 2; Length 101;
Best Local Similarity 60.0%; Pred. No. 9.4e-10;
Matches 24; Conservative 6; Mismatches 7; Indels 3; Gaps 2;

QY 1 ADCNG--ACSPFPPPC-RSRDCRCVPIGLFVGFCIHPTG 37
DB 26 ASCNGRDVCSPPFPPPCDDATNCRCIPWGLVVGQCVPSPG 65

RESULT 21
AL1C_PEA STANDARD; PRT; 130 AA.
ID AL1C_PEA
AC P62928; P08687; Q40999; Q7XZC0; Q9M3X4;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Albumin 1 C precursor (PA1 C) (PsaAlb015) [Contains: Albumin 1 C chain
DE B (PA1b C) (Leginulin C); Albumin 1 C chain a (PA1a C)].
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RA Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
RA Vallier A., Rahbe Y.;
RT "Molecular and biological screening for insect-toxic seed albumins
RT from four legume species.";
RL Plant Sci. 167:705-714(2004).
RN [2]
RP SEQUENCE OF 27-63, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC TISSUE=Seed;
RX MEDLINE=86278210; PubMed=3755437;
RA Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
RA Blagrove R.J., Kortt A.A., Inglis A.S.;
RT "Gene structure, protein structure, and regulation of the synthesis of
RT a sulfur-rich protein in pea seeds.";
RL J. Biol. Chem. 261:11124-11130(1986).
CC -I- FUNCTION: PALb binds to basic 7S globulin (BG) and stimulates its
CC phosphorylation activity. Involved in the signal transduction
CC system to regulate the growth and differentiation as a hormone
CC peptide. Toxic to various insects through binding to a high
CC affinity binding site in the insect gut (by similarity).
CC -I- TISSUE SPECIFICITY: Major component of both the cotyledons and
CC embryonic axes of mature seeds.
CC -I- DEVELOPMENTAL STAGE: Increasing expression during seed development
CC followed by a rapid degradation during the first days of seed
CC germination.
CC -I- PTM: The C-terminal glycine may be removed from PALb.
CC -I- MISCELLANEOUS: The protein sequenced in Ref.2 was probably a
CC mixture of the products of genes C and D, PALb being of C origin
CC while PALa is of D origin.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ574796; CAE00468.1; -.
DR InterPro; IPR011036; PH related.
KW Direct protein sequencing; Plant toxin; Seed storage protein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 63 Albumin 1 C chain b.
FT PROPEP 64 69
FT CHAIN 70 122 Albumin 1 C chain a.
FT PROPEP 123 130 Potential.
FT DISULFID 29 46 By similarity.
FT DISULFID 33 48 By similarity.

```

[illegible][illegible]

Search completed: March 28, 2005, 09:00:08  
Job time : 86 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2005, 08:50:15 ; Search time 23.5 Seconds  
(without alignments)  
151.490 Million cell updates/sec

Title: US-09-674-496d-8

Perfect score: 222

Sequence: 1 ADNGACSPFPPCRSDRCVPIGLFVGFCIRPTG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:\*

1: Pirl:\*

2: Pirl2:\*

3: Pirl3:\*

4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	119	2	S48192
2	155	69.8	130	2	A25014
3	63	28.4	3075	2	S14458
4	62.5	28.2	379	2	A59180
5	61.5	27.7	1847	2	T18308
6	59	26.6	3084	1	MMMSA
7	57.5	25.9	87	2	A39439
8	57.5	25.9	1018	2	T19693
9	57	25.7	88	2	JC5203
10	55.5	25.0	461	1	S18994
11	54.5	24.5	965	2	S62935
12	54	24.3	61	1	SMBO2
13	54	24.3	61	2	S00808
14	54	24.3	61	2	S00810
15	54	24.3	61	2	S00809
16	54	24.3	2195	2	T34284
17	53.5	24.1	371	2	T27643
18	53.5	24.1	1023	2	T30257
19	53.5	24.1	3507	2	T34513
20	53	23.9	61	2	A23889
21	53	23.9	140	2	T04904
22	53	23.9	295	2	A44984
23	53	23.9	3229	2	S27852
24	53	23.9	3566	1	A40701
25	53	23.9	4006	2	T09070
26	53	23.9	13288	2	T03099
27	52	23.4	130	1	KRSHA
28	52	23.4	435	2	I54182
29	52	23.4	582	2	T34538

30	52	23.4	820	2	G86246	hypothetical prote
31	51.5	23.2	340	2	T20148	probable cysteine
32	51	23.0	31	2	A59440	neurotoxin Bmk37 -
33	51	23.0	161	2	AD3462	hypothetical prote
34	51	23.0	174	2	B48454	cathepsin B-like c
35	51	23.0	304	2	T24703	hypothetical prote
36	51	23.0	561	1	A44128	(N-acetylneuraminy
37	51	23.0	593	1	GYHU	granulin precursor
38	51	23.0	1535	2	S46224	peroxidase - frui
39	50.5	22.7	62	2	S35098	trypsin inhibitor
40	50.5	22.7	90	2	B86560	9 kDa-Cysteine-ric
41	50.5	22.7	90	2	A72064	cysteine rich oute
42	50.5	22.7	1101	2	T16840	hypothetical prote
43	50.5	22.7	1104	2	T38869	transcription fact
44	50.5	22.7	1110	1	B42544	G2-G1 polyprotein
45	50.5	22.7	1188	2	D86236	protein F14N23.5 [
46	50	22.5	31	2	A59357	neurotoxin Bmk KTX
47	50	22.5	31	2	A59321	protein BmSKTx2 [i
48	50	22.5	48	1	A44664	omega-agatoxin IVB
49	50	22.5	61	2	T48173	metallothionein II
50	50	22.5	77	2	AD3531	hypothetical prote
51	50	22.5	273	2	B83489	probable binding p
52	50	22.5	404	2	JS0073	keratin, 47.6K typ
53	50	22.5	408	1	QRHUBE	beta-3-adrenergic
54	50	22.5	414	1	QRHUB3	beta-3-adrenergic
55	50	22.5	473	2	A56175	adhesive plaque pr
56	50	22.5	860	2	A96717	unknown protein, 4
57	49.5	22.3	57	2	A57537	guamerin - Korean
58	49.5	22.3	238	2	JQ2393	V protein - Newcas
59	49.5	22.3	1373	2	JS0095	gastric mucin MUC5
60	49.5	22.3	1639	1	MMFPB2	laminin gamma-1 ch
61	49	22.1	61	1	MMMS2	metallothionein II
62	49	22.1	61	2	I57572	metallothionein II
63	49	22.1	325	2	JN0148	necdin, brain - mo
64	49	22.1	418	2	G02953	beta-3-adrenergic
65	49	22.1	475	2	D88451	protein K10D2.2 [i
66	49	22.1	1124	1	I58388	protein-tyrosine k
67	49	22.1	1239	2	T13809	probable disintegr
68	49	22.1	1245	1	MMMSND	nidogen precursor
69	49	22.1	1506	2	T30886	integumentary muc
70	49	22.1	1574	2	T13954	MEGF6 protein - ra
71	49	22.1	3770	2	A40889	delta-(L-alpha-ami
72	48.5	21.8	63	2	S07127	chymotrypsin/elast
73	48.5	21.8	245	1	A47539	homeotic protein g
74	48.5	21.8	252	1	A54677	homeotic protein g
75	48.5	21.8	256	1	A42768	homeotic nicotinac
76	48.5	21.8	258	2	B36914	probable nicotinac
77	48.5	21.8	650	2	H81708	hypothetical prote
78	48.5	21.8	905	1	A27410	nucleotide diphosp
79	48.5	21.8	1106	2	T44598	hypothetical prote
80	48.5	21.8	1106	2	T13938	gene shuttle craft
81	48.5	21.8	1321	2	JE0352	mucin MUC5B, trach
82	48.5	21.8	1726	2	A39401	merozoite surface
83	48.5	21.8	1751	2	A45604	major blood-stage
84	48.5	21.8	1984	2	T13171	probable vitellog
85	48	21.6	43	2	S33382	metallothionein -
86	48	21.6	43	2	S18173	metallothionein -
87	48	21.6	43	2	S18174	metallothionein -
88	48	21.6	63	2	A34958	metallothionein -
89	48	21.6	63	2	S33381	metallothionein -
90	48	21.6	63	2	A34620	metallothionein -
91	48	21.6	63	2	C34620	metallothionein -
92	48	21.6	107	4	S57707	hypothetical prote
93	48	21.6	152	2	D95961	hypothetical prote
94	48	21.6	202	2	T50635	glutamate COA-tr
95	48	21.6	266	2	S51052	hypothetical prote
96	48	21.6	325	2	H71271	hypothetical prote
97	48	21.6	374	2	T18602	hypothetical prote
98	48	21.6	375	2	T16248	hypothetical prote
99	48	21.6	457	2	T46332	hypothetical prote
100	48	21.6	480	2	F84454	hypothetical prote

ALIGNMENTS

RESULT 1

S48192  
insulin-like growth factor S11 precursor - soybean  
N;Alternate names: leginsulin  
C;Species: Glycine max (soybean)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S48192; PNO116  
R;Katanabe, Y.; Barbashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunasawa, S.;  
Eur. J. Biochem. 224, 167-172, 1994  
A;Title: A peptide that stimulates phosphorylation of the plant insulin-binding protein.  
A;Reference number: S48192; MUID:94357216; PMID:8076638  
A;Accession: S48192  
A;Molecule type: mRNA; protein  
A;Residues: 1-119 <WAT>  
A;Cross-references: UNIPROT:Q39837; GB:D17396; NID:G498167; PIDN:BAA04219.1; PID:G498168  
R;Barbashov, S.F.; Egorov, T.A.  
Mol. Biol. (Mosk.) 24, 953-961, 1990  
A;Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cell g  
A;Reference number: PNO115; MUID:91066897; PMID:2250683  
A;Accession: PNO116  
A;Molecule type: protein  
A;Residues: 20-30,'M',32-39 <BAR>  
F;1-19/Domain: propeptide #status predicted <PRO>  
F;20-56/Product: insulin-like growth factor S11 #status experimental <MAT>

Query Match 100.0%; Score 222; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.3e-19;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADCNGACSPPEVPPCRRDCRCVPGLFVGFCIHPTG 37  
|||||  
Db 20 ADCNGACSPPEVPPCRRDCRCVPGLFVGFCIHPTG 56

RESULT 2

A25014  
albumin precursor - garden pea  
C;Species: Pisum sativum (garden pea)  
C;Date: 16-Aug-1998 #sequence\_revision 16-Aug-1998 #text\_change 09-Jul-2004  
C;Accession: A25014  
R;Higgins, T.J.V.; Chander, P.M.; Randall, P.J.; Spencer, D.; Beach, L.R.; Blagrove, R.  
J. Biol. Chem. 261, 11124-11130, 1986  
A;Title: Gene structure, protein structure, and regulation of the synthesis of a sulfur-  
A;Reference number: A25014; MUID:86278210; PMID:3755437  
A;Accession: A25014  
A;Molecule type: DNA  
A;Residues: 1-130 <HIG>  
A;Cross-references: UNIPROT:P08687; GB:M13709; NID:G169024; PIDN:AAA33638.1; PID:G169025  
C;Genetics:  
A;Introns: 17/1  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-130/Product: albumin #status predicted <MAT>

Query Match 69.8%; Score 155; DB 2; Length 130;  
Best Local Similarity 62.2%; Pred. No. 1.3e-11;  
Matches 23; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ADCNGACSPPEVPPCRRDCRCVPGLFVGFCIHPTG 37  
|||||  
Db 27 ASCNGVCSPPEMPPCGTACRCIPVGLVVGCRNPSG 63

RESULT 3

S14458  
laminin alpha-1 chain precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: S14458; S14663; A34961  
R;Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.  
Matrix 11, 151-160, 1991

A;Title: Molecular cloning of the cDNA encoding human laminin A chain.  
A;Reference number: S14458; MUID:91333420; PMID:1714537  
A;Accession: S14458  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-3075 <HAA>  
A;Cross-references: UNIPROT:P25391  
R;Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.  
Biochem. J. 276, 369-379, 1991  
A;Title: Primary structure of the human laminin A chain. Limited expression in human tis  
A;Reference number: S14663; MUID:91264789; PMID:2049067  
A;Accession: S14663  
A;Molecule type: mRNA  
A;Residues: 1-227,'FE',230-251,'MLP',255-418,'E',420-518,'L',520-1022,'V',1024-1074,'V',1  
A;Cross-references: EMBL:X58531; NID:G34225; PIDN:CAA41418.1; PID:G34226  
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T.  
Lab. Invest. 60, 772-782, 1989  
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A;Reference number: A34961; MUID:89280632; PMID:2733383  
A;Accession: A34961  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS>  
A;Note: the authors translated the codon AGA for residue 2692 as Pro  
C;Genetics:  
A;Gene: GDB:LAMAL1; LAMA  
A;Cross-references: GDB:120135; OMIM:150320  
A;Map position: 18p11.32-18p11.22  
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hom  
C;Keywords: Basement membrane; calcium binding; cell binding; coiled coil; disulfide bon  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>  
F;18-269/Domain: VI <DOM6>  
F;270-516/Domain: V <DOM5>  
F;270-324/Domain: laminin-type EGF-like homology <LE1>  
F;327-394/Domain: laminin-type EGF-like homology <LE2>  
F;397-451/Domain: laminin-type EGF-like homology <LE3>  
F;454-500/Domain: laminin-type EGF-like homology <LE4>  
F;503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>  
F;517-708/Domain: IIV <DO4B>  
F;709-1159/Domain: IIIB <DO3B>  
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>  
F;742-788/Domain: laminin-type EGF-like homology <LE7>  
F;791-846/Domain: laminin-type EGF-like homology <LE8>  
F;849-899/Domain: laminin-type EGF-like homology <LE9>  
F;902-948/Domain: laminin-type EGF-like homology <LE10>  
F;951-995/Domain: laminin-type EGF-like homology <LE11>  
F;998-1041/Domain: laminin-type EGF-like homology <LE12>  
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>  
F;1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>  
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>  
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>  
F;1160-1361/Domain: IVA <DO4A>  
F;1362-1553/Domain: IIIfa <DO3A>  
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>  
F;1403-1449/Domain: laminin-type EGF-like homology <LE18>  
F;1452-1506/Domain: laminin-type EGF-like homology <LE19>  
F;1509-1553/Domain: laminin-type EGF-like homology <LE20>  
F;1554-2125/Domain: I/II, heptad repeats <DOM2>  
F;2116-2120/Region: cell adhesion #status predicted  
F;2126-3075/Domain: G <DOMG>  
F;2142-2300/Domain: laminin G repeat homology <LG1>  
F;2329-2484/Domain: laminin G repeat homology <LG2>  
F;2510-2676/Domain: laminin G repeat homology <LG3>  
F;2534-2536/Region: cell attachment (R-G-D) motif  
F;2739-2888/Domain: laminin G repeat homology <LG4>  
F;2916-3073/Domain: laminin G repeat homology <LG5>  
F;381,164,555,665,763,801,838,926,1045,1407,1579,1596,1678,1689,1717,1804,1894,1  
rate (Asn) (covalent) #status predicted  
F;297-305/Disulfide bonds: #status predicted

Query Match 28.4%; Score 63; DB 2; Length 3075;  
Best Local Similarity 46.2%; Pred. No. 15;





QY 2 DC-NGACSPFEVPPC-RSRDRCVPIGLFGVGFIHTPG 37  
 ||| :|| :|| :|| :|| :|| :||  
 Db 25 DCCFEDCAPKPCNFCGNKKDKGCSGPCGVYTFSCKPCG 63

RESULT 8  
 T19693  
 hypothetical protein C34B7.1 - Caenorhabditis elegans  
 C;Species:Caenorhabditis elegans  
 C;Date:15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession:T19693  
 R;Harris, B.  
 submitted to the EMBL Data Library, December 1996  
 A;Reference number: Z19165  
 A;Accession:T19693  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1018 <WIL>  
 A;Cross-references: UNIPROT:P90769; EMBL:Z83220; PIDN:CAB05700.1; GSPDB:GNO  
 A;Experimental source: clone C34B7  
 C;Genetics:  
 A;Gene: CESP:C34B7.1  
 A;Map position: 1  
 A;Introns: 78/1; 149/1; 177/1; 245/1; 311/2; 361/2; 387/3; 415/2; 44

Query Match 25.9%; Score 57.5; DB 2; Length 1018;  
 Best Local Similarity 32.4%; Pred. No. 29;  
 Matches 12; Conservative 2; Mismatches 16; Indels 7; Gaps

QY 3 CNGACSPFEVPPCSR-----DCRCVPIGLFGVGC 32  
 ||| :|| :|| :|| :|| :|| :||  
 Db 133 CNNYCNPQTPIPQRPLVRVCDSDDSCFTGSC 169

RESULT 9  
 JC5203  
 outer membrane protein 3 precursor - Chlamydomophila psittaci  
 C;Species:Chlamydomophila psittaci, Chlamydia psittaci  
 C;Date:20-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 31-Mar-2000  
 C;Accession:JC5203  
 R;Hsia, R.; Bavofil, P.M.  
 Gene 176, 155-162, 1996  
 A;Title: Sequence analysis of the omp2 region of Chlamydia psittaci strain  
 A;Reference number: JC5203; MUID:97075924; PMID:8918247  
 A;Accession:JC5203  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-88 <HSI>  
 A;Cross-references: GB:U41759; NID:g1783376; PIDN:AAB41142.1; PID:g1783381  
 A;Experimental source: strain GPIC  
 C;Genetics:  
 A;Gene: omp3  
 F;1-19/Domain: signal sequence #status predicted <SIG>

Query Match 25.7%; Score 57; DB 2; Length 88;  
 Best Local Similarity 32.5%; Pred. No. 4.9;  
 Matches 13; Conservative 3; Mismatches 20; Indels 4; Gaps

QY 2 DC-NGACSPFEVPPCR--SRDRCVPIGLFGVGFIHTPG 37  
 ||| :|| :|| :|| :|| :|| :||  
 Db 25 DCCFEDCAPKPCNFCNVFKDGECSCGSYTFSCSKPCG 64

RESULT 10  
 S18994  
 protein C (activated) (EC 3.4.21.69) precursor - rat  
 C;Species:Rattus norvegicus (Norway rat)  
 C;Date:10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession:S18994; S24312  
 R;Okafuji, T.; Maekawa, K.; Nawata, K.; Marumoto, Y.  
 submitted to the EMBL Data Library, February 1992  
 A;Description: The cDNA cloning and mRNA expression of rat protein C.  
 A;Reference number: S18994

A;Accession: S18994  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-461 <OKA>  
A;Cross-references: UNIPROT:P31394; EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963  
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
Biochim. Biophys. Acta 1131, 329-332, 1992  
A;Title: The cDNA cloning and mRNA expression of rat protein C.  
A;Reference number: S24312; MUID:92329550; PMID:1627650  
A;Accession: S24312  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-461 <OKA2>  
A;Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
F;1-32/Domain: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase  
F;27-85/Domain: signal sequence #status predicted <SIG>  
F;33-42/Domain: Gla domain homology <GLA>  
F;43-461/Product: propeptide #status predicted <PRO>  
F;91-130/Domain: product: protein C #status predicted <PRC>  
F;139-174/Domain: EGF homology <EG1>  
F;213-445/Domain: trypsin homology <TRY>  
F;47, 48, 55, 57, 60, 61, 66, 67, 70, 76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat  
F;215,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 25.0%; Score 55.5; DB 1; Length 461;  
Best Local Similarity 42.3%; Pred. No. 27;  
Matches 11; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

Qy 2 DC---NGACSPFVEVPPCRSDRCVCP 24  
||| ||| : : : ||| |||  
Db 138 DCRVNGGCVHYCLEETRRRCRCAP 163

RESULT 11  
S62935  
hypothetical protein YNL023c - Yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein N2812  
C;Species: Saccharomyces cerevisiae  
C;Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
C;Accession: S62935; S62945  
R;Andre, B.; Iragui Housaini, I.; Urrestarazu, L.A.; Vissers, S.  
submitted to the Protein Sequence Database, April 1996  
A;Reference number: S62920  
A;Accession: S62935  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-965 <AND>  
A;Cross-references: UNIPROT:P53971; EMBL:Z71299; NID:G1301854; PID:e239870; PID:G1301855  
A;Experimental source: strain S288C  
R;Duisterhoft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
submitted to the Protein Sequence Database, April 1996  
A;Reference number: S62944  
A;Accession: S62945  
A;Molecule type: DNA  
A;Residues: 1-965 <DUE>  
A;Cross-references: EMBL:Z71299; NID:G1301854; PID:e239870; PID:G1301855; MIPS:YNL023C  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:FAP1  
A;Cross-references: SGD:S0004968  
A;Map position: 14L

Query Match 24.5%; Score 54.5; DB 2; Length 965;  
Best Local Similarity 30.4%; Pred. No. 64;  
Matches 14; Conservative 2; Mismatches 17; Indels 13; Gaps 2;

Qy 3 CNGACSPFVEVPPCRSD-----CRC-----VPIGLFVGCFCIHP 35  
||| ||| : : : ||| |||  
Db 473 CQRKCHFGKCPCLSDSLVCPGNTVWPAPVRCGKLTCTNHP 518

RESULT 12  
SMB02  
metallothionein II - bovine  
N;Alternate names: MT-II  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C;Accession: A03279  
R;Winge, D.R.; Gray, W.R.; Zelazowski, A.; Garvey, J.S.  
Arch. Biochem. Biophys. 245, 254-262, 1986  
A;Title: Sequence and antigenicity of calf metallothionein II.  
A;Reference number: A03279; MUID:86129456; PMID:3947100  
A;Accession: A03279  
A;Molecule type: protein  
A;Residues: 1-61 <WIN>  
A;Cross-references: UNIPROT:P04356  
A;Experimental source: calf liver  
A;Note: 49-Ile was also found  
C;Comment: The vertebrate metallothioneins contain two metal-binding domains. Clusters o  
C;Superfamily: metallothionein  
C;Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster  
F;1-29/Domain: beta <NH2>  
F;30-61/Domain: alpha <MLP>  
F;1/Modified site: acetylated amino end (Met) #status experimental  
F;5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted  
F;33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre

Query Match 24.3%; Score 54; DB 1; Length 61;  
Best Local Similarity 34.6%; Pred. No. 8.4;  
Matches 9; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 3 CNGACSPFVEVPPCRSDRCVPIG 26  
||| ||| : : : ||| |||  
Db 15 CAGSCTCKACRCPCKKSCGCCCPVG 40

RESULT 13  
S00808  
metallothionein Ia - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: S00808; I46414; I46559  
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.  
Eur. J. Biochem. 174, 417-424, 1988  
A;Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel  
A;Reference number: S00808; MUID:88254812; PMID:3383853  
A;Accession: S00808  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-61 <PET1>  
A;Cross-references: UNIPROT:P04356; GB:X04626; NID:G4218467; PIDN:CAA28299.1; PID:G42184  
R;Peterson, M.G.; Mercer, J.F.  
Eur. J. Biochem. 160, 579-585, 1986  
A;Title: Structure and regulation of the sheep metallothionein-Ia gene.  
A;Reference number: I46414; MUID:87053978; PMID:3780723  
A;Accession: I46414  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-49, S, 51-61 <PET2>  
A;Cross-references: EMBL:X04626; NID:G4218467  
R;Peterson, M.G.; Lazdins, I.; Danks, D.M.; Mercer, J.F.  
Eur. J. Biochem. 143, 507-511, 1984  
A;Title: Cloning and sequencing of a sheep metallothionein cDNA.  
A;Reference number: I46559; MUID:85003624; PMID:6434305  
A;Accession: I46559  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-61 <PET3>  
A;Cross-references: EMBL:X00953; NID:G1825; PIDN:CAA25464.1; PID:G1826  
C;Genetics:  
A;Introns: 10/1; 32/1



A:Map position: 4  
A:Introns: 26/1; 73/1  
A:Note: T10114.60

Query Match 23.9%; Score 53; DB 2; Length 140;  
Best Local Similarity 31.2%; Pred. No. 21;  
Matches 10; Conservative 6; Mismatches 6; Indels 10; Gaps 2;

Qy 5 GACSPFE-----VPCRSRDC-----RCVPIG 26  
| | | | | : | | | | | | | | | |  
Db 38 GECNSYEKSTCIEPCKQLDCKFIGRCIPVG 69

RESULT 22  
A44984  
collagen - nematode (Haemonchus contortus)  
C:Species: Haemonchus contortus  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 15-Sep-2003  
C:Accession: A44984  
R:Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N.  
Mol. Biochem. Parasitol. 37, 73-86, 1989  
A:Title: Cuticle collagen genes of Haemonchus contortus and Caenorhabditis elegans are h  
A:Reference number: A44984; MUID:90136718; PMID:2615789  
A:Accession: A44984  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-295 <SHA>  
A:Cross-references: GB:J04670

Query Match 23.9%; Score 53; DB 2; Length 295;  
Best Local Similarity 39.1%; Pred. No. 38;  
Matches 9; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 NGACSPFEVPPCRSRDCRCVPIG 26  
| | | | | : | | | | | | | | | |  
Db 130 DGSCEPVSIPPC--AECNAGPPG 150

RESULT 23  
S27852  
probable cell-surface protein (cysteine-rich repeat motif) - Trypanosoma cruzi  
N:Alternate names: hypothetical protein DGF-1  
C:Species: Trypanosoma cruzi  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: A48450; S27852  
R:Wincker, P.; Murto-Dovales, A.C.; Goldenberg, S.  
Mol. Biochem. Parasitol. 55, 217-220, 1992  
A:Title: Nucleotide sequence of a representative member of a Trypanosoma cruzi dispersed  
A:Reference number: A48450; MUID:93063053; PMID:1435871  
A:Accession: A48450  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-3229 <W12>  
A:Cross-references: UNIPROT:Q26912; EMBL:M90534; NID:g162051; PID:g162052  
A:Note: sequence extracted from NCBI backbone (NCBIP:118407)  
C:Superfamily: Trypanosoma cruzi probable cell-surface protein (cysteine-rich repeat motif)

Query Match 23.9%; Score 53; DB 2; Length 3229;  
Best Local Similarity 69.2%; Pred. No. 2.5e+02;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ACSPPFEVPPCRSR 18  
| | | | | : | | | | | | | | | |  
Db 260 ACLPFDVPPARPR 272

RESULT 24  
A40701  
tenascin-X precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A40701; A33725; C42175  
R:Bristow, J.; Tee, M.K.; Gicelman, S.E.; Mellon, S.H.; Miller, W.L.

J. Cell Biol. 122, 265-278, 1993  
A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene  
A;Reference number: A40701; MUID:93300909; PMID:7686164  
A;Accession: A40701  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-3566 <BRI>  
A;Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; EMBL:X71937  
R;Morel, Y.; Brietow, J.; Gitelman, S.E.; Miller, W.L.  
Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989  
A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/  
A;Reference number: A33725; MUID:89367293; PMID:2475872  
A;Accession: A33725  
A;Molecule type: mRNA  
A;Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>  
A;Cross-references: GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:g183070  
R;Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.  
Genomics 12, 485-491, 1992  
A;Title: Cluster of fibronectin type III repeats found in the human major histocompatibility  
enascin.  
A;Reference number: A42175; MUID:92217969; PMID:1373119  
A;Accession: A42175  
A;Molecule type: DNA  
A;Residues: 1849-1936 <MAT>  
A;Experimental source: clone 3.9kF3-1  
A;Note: sequence extracted from NCBI backbone (NCBIP:95694)  
C;Genetics:  
A;Gene: GDB:TNXA; D6S103E; TNX; XA; XB  
A;Cross-references: GDB:568487; OMIM:600261  
A;Map position: 9p21.3-9p21.3  
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
C;Keywords: extracellular matrix; glycoprotein  
F;435-461/Domain: EGF homology <EGF>  
F;748-828/Domain: fibronectin type III repeat homology <3F1>  
F;829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>  
F;873-953/Domain: fibronectin type III repeat homology <3F3>  
F;975-1055/Domain: fibronectin type III repeat homology <3F4>  
F;1078-1158/Domain: fibronectin type III repeat homology <3F5>  
F;1167-1247/Domain: fibronectin type III repeat homology <3F6>  
F;1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7>  
F;1323-1403/Domain: fibronectin type III repeat homology <3F8>  
F;1412-1492/Domain: fibronectin type III repeat homology <3F9>  
F;1510-1590/Domain: fibronectin type III repeat homology <3F10>  
F;1618-1676/Domain: fibronectin type III repeat homology #status atypical <3F11>  
F;1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12>  
F;1751-1831/Domain: fibronectin type III repeat homology <3F13>  
F;1849-1929/Domain: fibronectin type III repeat homology <3F14>  
F;1955-2035/Domain: fibronectin type III repeat homology <3F15>  
F;2061-2141/Domain: fibronectin type III repeat homology <3F16>  
F;2167-2246/Domain: fibronectin type III repeat homology <3F17>  
F;2274-2354/Domain: fibronectin type III repeat homology <3F18>  
F;2382-2462/Domain: fibronectin type III repeat homology <3F19>  
F;2488-2568/Domain: fibronectin type III repeat homology <3F20>  
F;2584-2664/Domain: fibronectin type III repeat homology <3F21>  
F;2677-2757/Domain: fibronectin type III repeat homology <3F22>  
F;2771-2851/Domain: fibronectin type III repeat homology <3F23>  
F;2878-2958/Domain: fibronectin type III repeat homology <3F24>  
F;2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25>  
F;3078-3159/Domain: fibronectin type III repeat homology <3F26>  
F;3167-3247/Domain: fibronectin type III repeat homology <3F27>  
F;3255-3334/Domain: fibronectin type III repeat homology <3F28>  
F;3349-3557/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 23.9%; Score 53; DB 1; Length 3566;  
Best Local Similarity 47.6%; Pred.No. 2.7e+02;  
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 3 CNGACSPFEVPCRSRDCRCV 23

Db 688 CPGGCGPREL--CRAGQCVCV 706

RESULT 25

T09070  
probable tenascin X - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09070  
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Loretz, C.; Sci  
submitted to the EMBL Data Library, October 1997  
A;Description: Sequence of the mouse major histocompatibility locus class III region.  
A;Reference number: Z16543  
A;Accession: T09070  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-4006 <ROW>  
C;Genetics:  
A;Gene: TNX  
A;Map position: 17  
A;Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15  
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3  
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
C;Keywords: extracellular matrix  
F;422-448/Domain: EGF homology <EGF>  
F;826-906/Domain: fibronectin type III repeat homology <3FR>  
F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>  
Query Match 23.9%; Score 53; DB 2; Length 4006;  
Best Local Similarity 47.6%; Pred.No. 3e+02;  
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;  
QY 3 CNGACSPFEVPCRSRDCRCV 23  
Db 675 CPGGCGPREL--CRAGQCVCV 693  
Search completed: March 28, 2005, 09:01:07  
Job time : 25.5 secs







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; PRIOR FILING DATE: 1988-11-02
; PRIOR APPLICATION NUMBER: US 06/692,605
; PRIOR FILING DATE: 1985-01-17
; PRIOR APPLICATION NUMBER: US 07/582,241
; PRIOR FILING DATE: 1990-09-14
; PRIOR APPLICATION NUMBER: US 07/188,361
; PRIOR FILING DATE: 1988-04-29
; PRIOR APPLICATION NUMBER: US 07/168,190
; PRIOR FILING DATE: 1988-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protease
; OTHER INFORMATION: Inhibitor Palb peptide sequence
US-09-782-130-12

Query Match      34.2%; Score 76; DB 11; Length 18;
Best Local Similarity 64.7%; Pred. No. 0.057;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

-Qy      7 CSPPEVPPCRSRDCRCV 23
        ||||:|||||
Db      2 CSPFDIPCGSPLCRCI 18

RESULT 5
US-10-424-599-272087
; Sequence 272087, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272087
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87713C.1.pep
US-10-424-599-272087

Query Match      30.9%; Score 68.5; DB 15; Length 79;
Best Local Similarity 45.7%; Pred. No. 1.5;
Matches 16; Conservative 2; Mismatches 10; Indels 7; Gaps 2;

-Qy      1 ADCNGACS--PFEVPP-----PCSRDCRCVPIGLF 28
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      23 SQCSGGCSQTFFPKPCLFFFPFKCSKCLCVPPGPF 57

RESULT 6
US-09-764-868-653
; Sequence 653, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
```

```
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 653
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-653

Query Match      30.2%; Score 67; DB 9; Length 158;
Best Local Similarity 32.6%; Pred. No. 4;
Matches 14; Conservative 5; Mismatches 14; Indels 10; Gaps 1;

-Qy      5 GACSPFEVPPCRSRDCRCVPIGLFVGFC-----IHPTG 37
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      96 GGOQPSQPPPARASQCPSLSQLFLGFCQLVGPPTCALHPRG 138

RESULT 7
US-09-938-275-5
; Sequence 5, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; FILE REFERENCE: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3075
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P25391
; DATABASE ENTRY DATE: 1992-05-01
US-09-938-275-5

Query Match      28.4%; Score 63; DB 9; Length 3075;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

-Qy      8 SPFEVPPCRSRDCRCVPIGLFVGFCI 33
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      387 SPVEDEPC--RPCNCDPVGSLSSVCI 410

RESULT 8
US-10-437-963-187490
; Sequence 187490, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187490
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_84188C.1.pep  
US-10-437-963-187490

Query Match 28.2%; Score 62.5; DB 16; Length 77;  
Best Local Similarity 46.2%; Pred. No. 7;  
Matches 12; Conservative 0; Mismatches 9; Indels 5; Gaps 1;

QY 2 DCNGA-----CSPFEVPPCRSRDCRC 22

Db 50 DCKAAGLTAVCPVPVPPRCRRSRDCRC 75

## RESULT 9

US-10-357-820-20  
; Sequence 20, Application US/10357820  
; Publication No. US20040029140A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David W.;  
; APPLICANT: Burgess, Catherine E.;  
; APPLICANT: Casman, Stacie J.;  
; APPLICANT: Gorman, Linda;  
; APPLICANT: Ji, Weizhen;  
; APPLICANT: Kekuda, Ramesh;  
; APPLICANT: Li, Li;  
; APPLICANT: Padisaru, Muralidhara;  
; APPLICANT: Patturajan, Meera;  
; APPLICANT: Pena, Carol E.A.;  
; APPLICANT: Shenoy, Suresh G.;  
; APPLICANT: Shimkets, Richard A.;  
; APPLICANT: Stone, David J.;  
; APPLICANT: Taupier, Raymond J.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, AND METHOD  
; FILE REFERENCE: 21402-538B

**TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS**

```

; CURRENT APPLICATION NUMBER: US/10/357,820
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/381666
; PRIOR FILING DATE: 2002-05-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 337

```

ORGANISM: Homo sapiens  
US-10-357-820-20

Query Match 28.2%; Score 62.5; DB 15; Length 337;  
Best Local Similarity 33.9%; Pred. No. 25;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

1 ADNGAC-----SPFEVPPCRSDC--RCVPIGLEV--GFCIHPTG 37  
152 AECPPGCRNGGFCNERRICECPDGFHGFHCEKALCTPRCWNGGLCTVPGFCICPPG 207

## RESULT 10

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US-10-357-820-8
; Sequence 8, Application US/10357820
; Publication NO. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padigar, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Penda, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shinkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC POLYMER
; FILE REFERENCE: 21402-536B
; CURRENT APPLICATION NUMBER: US/10/373-03
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679466
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730611
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/381666
; PRIOR FILING DATE: 2002-05-17
; Remaining Prior Application data re:
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Curaseqseq version 0.1
; SEQ ID NO 8
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-8

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Query Match      28.2%; Score 62.5; DB 15; Length 343;
Best Local Similarity 33.9%; P: Nsmat0.26;
Matches 19; Conservative 16; Mismatches 16; Indels 19; Gaps 3;
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RESULT 11

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US-103-357-820-4
; Sequence 4: Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Scatce J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Rameesh;
; APPLICANT: Li, Li;

```

```

RESULT 12
US/10-357-820-6
; Sequence 6, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgeess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weisheng;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padgaru, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Pena, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shinkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC PO
; FILE REFERENCE: 21402-538B
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/67946

```

```

RESULT 13
US-10-357-820-10
, Sequence 10, Application US/10357820
, Publication No. US20040029140A1
, GENERAL INFORMATION:
, APPLICANT: Anderson, David W.;
, APPLICANT: Burgess, Catherine E.;
, APPLICANT: Casman, Scacette J.;
, APPLICANT: Gorman, Linda;
, APPLICANT: Ji, Weizhen;
, APPLICANT: Kekuda, Ramesh;
, APPLICANT: Li, Li;
, APPLICANT: Padigaru, Muralidhara;
, APPLICANT: Patturajan, Meera;
, APPLICANT: Pena, Carol E.A.;
, APPLICANT: Shenoy, Suresh G.;
, APPLICANT: Shmukes, Richard A.;
, APPLICANT: Stone, David J.;
, APPLICANT: Taupier, Raymond J.
, TITLE OF INVENTION: THERAPEUTIC POL
, FILE REFERENCE: 21402-538B
, CURRENT APPLICATION NUMBER: US/10/3
, CURRENT FILING DATE: 2003-02-03
, PRIOR APPLICATION NUMBER: 09/679460
, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: 09/730617
, PRIOR FILING DATE: 2000-12-05
, PRIOR APPLICATION NUMBER: 10/074978
, PRIOR FILING DATE: 2002-02-12
, PRIOR APPLICATION NUMBER: 10/138588
, PRIOR FILING DATE: 2002-05-01
, PRIOR APPLICATION NUMBER: 60/387002
, PRIOR FILING DATE: 2002-06-07
, PRIOR APPLICATION NUMBER: 60/355099
, PRIOR FILING DATE: 2002-02-08
, PRIOR APPLICATION NUMBER: 60/375579

```

```
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/381666
; PRIOR FILING DATE: 2002-05-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 10
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-10

Query Match      28.2%; Score 62.5; DB 15; Length 373;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 185 AECPGGCRNGGFCNERRICECPDGFHGHPCHEKALCTPRCWMNGGLCVTPGFCICPPG 240

RESULT 14
US-10-357-820-12
; Sequence 12, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padigar, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Pena, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538B
; CURRENT APPLICATION NUMBER: US/10/357,820
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/381666
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-10

Query Match      28.2%; Score 62.5; DB 15; Length 373;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 185 AECPGGCRNGGFCNERRICECPDGFHGHPCHEKALCTPRCWMNGGLCVTPGFCICPPG 240

RESULT 15
US-10-357-820-18
; Sequence 18, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padigar, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Pena, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538B
; CURRENT APPLICATION NUMBER: US/10/357,820
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/381666
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 18
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-18

Query Match      28.2%; Score 62.5; DB 15; Length 377;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 176 AECPGGCRNGGFCNERRICECPDGFHGHPCHEKALCTPRCWMNGGLCVTPGFCICPPG 231
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-12

Query Match      28.2%; Score 62.5; DB 15; Length 375;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 176 AECPGGCRNGGFCNERRICECPDGFHGHPCHEKALCTPRCWMNGGLCVTPGFCICPPG 231

RESULT 15
US-10-357-820-18
; Sequence 18, Application US/10357820
; Publication No. US20040029140A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Casman, Stacie J.;
; APPLICANT: Gorman, Linda;
; APPLICANT: Ji, Weizhen;
; APPLICANT: Kekuda, Ramesh;
; APPLICANT: Li, Li;
; APPLICANT: Padigar, Muralidhara;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Pena, Carol E.A.;
; APPLICANT: Shenoy, Suresh G.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Stone, David J.;
; APPLICANT: Taupier, Raymond J.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538B
; CURRENT APPLICATION NUMBER: US/10/357,820
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/679460
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/730617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 10/074978
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 10/138588
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/387002
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/355099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/375579
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/393265
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 401825
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/381666
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 18
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-820-18

Query Match      28.2%; Score 62.5; DB 15; Length 377;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 176 AECPGGCRNGGFCNERRICECPDGFHGHPCHEKALCTPRCWMNGGLCVTPGFCICPPG 231
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-4

Query Match      28.2%; Score 62.5; DB 9; Length 379;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps

QY 1 ADNGAC-----SPFEVPCRRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGCGRRGFCNERRICECPDGFHPCERKALCTPRCWNGGLCVTPGFCICPPG 235

RESULT 17
US-09-909-088B-4
; Sequence 4, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379

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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-4

Query Match      28.2%; Score 62.5; DB 9; Length 379;
Best Local Similarity 33.9%; Pred. No. 28;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps

QY      1  ADCNGAC-----SPPEVPPCRSRDC--RCVPIGLFLV--GFCIHPTG 37
DB      180  AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCWGGLCVTPGFCICPPG 235

RESULT 19
US-09-902-853-4
; Sequence 4, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350

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Publication No. US20030023054A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906,742  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
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PRIOR APPLICATION NUMBER: PCT/US99/28564  
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PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 4  
LENGTH: 379  
TYPE: PRT  
ORGANISM: Homo Sapien

US-09-906-742-4  
Query Match 28.2%; Score 62.5; DB 10; Length 379;  
Best Local Similarity 33.9%; Pred. No. 28;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;  
QY 1 ADCNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37  
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Job time : 68.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
92.067 Million cell updates/sec

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	63	28.4	243	2	US-08-125-077-15
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5	62.5	28.2	379	4	US-09-907-794A-4
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7	62.5	28.2	379	4	US-09-902-775A-4
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53	51	23.0	593	1	US-07-668-648-4	Sequence 4, Appl
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96	49	22.1	135	4	US-09-252-991A-26163	Sequence 26163, A
97	49	22.1	131	4	US-09-252-991A-21561	Sequence 21561, A
98	49	22.1	210	4	US-09-252-991A-30732	Sequence 30732, A
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; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-125-077-5

Query Match      28.4%; Score 63; DB 2; Length 3075;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY      8 SPFEVPPCRSDRCRCVPICGLFVGFGCI 33
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DB      387 SPYEDEPC--RPCNCDPVGLSSVCII 410

RESULT 5
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; Sequence 4, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER:..US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15

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, PRIOR APPLICATION NUMBER: US 60/145,698
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, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 4
, LENGTH: 379

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Query Match      28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred. NO. 9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

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; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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US-09-603A-4
; Sequence 4, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.16182C12
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/903.603A
; PRIOR FILING DATE: 2000-02-22 PCT/US00/04414
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-603A-4
Query Match 28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred. No. 9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCRSRTC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGGFCNERRICPCDPGFHGHPCHEKALCTPRCMNGGLCVTFPGFCICPPG 235

RESULT 10
US-09-904-920A-4
; Sequence 4, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/904,920A
; PRIOR FILING DATE: 2000-02-22 PCT/US00/04414
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

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; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 4  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-920A-4

Query Match 28.2%; Score 62.5; DB 4; Length 379;  
Best Local Similarity 33.9%; Pred. No. 9.6;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADGNGAC-----SPFEVPPCERSDC--RCVPIGLFV--GFCIHPTG 37  
Db 180 AECFGGCRNGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTFGFCICPPG 235

## RESULT 11

US-09-909-064-4

; Sequence 4, Application US/09909064  
; Patent No. 6818449  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US/09/909,064  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 4  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-909-064-4

Query Match 28.2%; Score 62.5; DB 4; Length 379;  
Best Local Similarity 33.9%; Pred. No. 9.6;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADGNGAC-----SPFEVPPCERSDC--RCVPIGLFV--GFCIHPTG 37  
Db 180 AECFGGCRNGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTFGFCICPPG 235

## RESULT 12

US-09-905-381A-4

; Sequence 4, Application US/09905381A  
; Patent No. 6818746  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US/09/905,381A  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048

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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 4
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-381A-4

      28.2%   Score 62.5; DB 4; Length 379;
Best Match   33.9%; Pred No. 9.6;
Query Local Similarity
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADNGAC-----SPFEVPPCKSRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECPGGCRNGGFCNERRICEPCDGFHGHFCEKALCTPRCMNGGLCVTPGFCICPPG 235

RESULT 13
US-09-906-618-4
; Sequence 4, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøtttsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Rev. Margaret Ann

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; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 441
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (264)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (380)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-205-258-441

Query Match      28.2%   Score 62.5; DB 4; Length 380;
Best Local Similarity 33.9%; Pred.No.9.7; Mismatches 16; Indels 19; Gaps 3;
Matches 19; Conservative 2;

Qy 1 ADGNGAC-----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
Db 180 AECFGGCRNGGFCNERRICPCDGFHGHKEKALCTPRCMNGGLCVTPGFCICPPG 235

RESULT 15
US-08-460-309-16
; Sequence 16, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17820
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa

Query Match      25.0%; Score 55.5; DB 4; Length 195;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 14; Conservative 1; Mismatches 10; Indels 7; Gaps 2;

Qy 1 ADCNGA-----CGPFEVPPCR-SRDCRCVPI 25
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Db 142 ASCSTATAPVACCSATPVPPCRASPSANCTPI 173

RESULT 20
US-09-252-991A-26035
; Sequence 26035, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Matc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26035
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26035

Query Match      25.0%; Score 55.5; DB 4; Length 249;
Best Local Similarity 51.9%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 8; Indels 3; Gaps 2;

Qy 3 CNG--ACSPFEVPP-CRSRDCRCVPIG 26
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Db 136 CRGRDRAGSPGVPPGCRADCCQSPG 162

RESULT 21
US-09-538-092-650
; Sequence 650, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqFormatter Version 0.9
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; SEQ ID NO 650
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YNL023C
US-09-538-092-650

Query Match      24.5%; Score 54.5; DB 4; Length 965;
Best Local Similarity 30.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 17; Indels 13; Gaps 2;

Qy 3 CNGACSPFEVPPCRSRD-----CRC-----VPIGLFVGFCIHP 35
| | | | | | | | | | | | | | | | | |
Db 473 CQRKCHPGKPPCLESNSDLVCPGTVVVPAPVRCGKLTPTCNHP 518

RESULT 22
US-09-270-767-34799
; Sequence 34799, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34799
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; ORGANISM: Drosophila melanogaster

US-09-270-767-34799

Query Match      24.3%; Score 54; DB 4; Length 178;
Best Local Similarity 39.4%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 15; Indels 2; Gaps 2;

Qy 1 ADCNGACSPFEVP-PCRSRDCRCVPIGLFGVFC 32
| | | | | | | | | | | | | | | |
Db 142 AGAAACHPAQIPGGCIGRCHCLGIGR-PGLC 173

RESULT 23
US-09-270-767-50016
; Sequence 50016, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50016
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; ORGANISM: Drosophila melanogaster

US-09-270-767-50016

Query Match      24.3%; Score 54; DB 4; Length 178;
Best Local Similarity 39.4%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 15; Indels 2; Gaps 2;

Qy 1 ADCNGACSPFEVP-PCRSRDCRCVPIGLFGVFC 32
| | | | | | | | | | | | | | | |
Db 142 AGAAACHPAQIPGGCIGRCHCLGIGR-PGLC 173
```

RESULT 24

```

RESULT 24
US-09-232-191-19
; Sequence 19, Application US/09232191
; Patent No. 6284487
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Fatty Acid Transport Proteins
; FILE REFERENCE: WHI97-21p3ME
; CURRENT APPLICATION NUMBER: US/09/232,191
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-191-19

Query Match          24.3%; Score 54; DB 3; Length 199;
Best Local Similarity 28.6%; Pred. No. 50;
Matches 16; Conservative 5; Mismatches 7; Indels 28; Gaps 3;

```

Qy	4	NGAC	SPFEV	PPCRSDRCVPIGL	-----	FVGF	31
	:	:	:	:	:	:	:
Db	22	DGACLLRMLS	PFELVDFOMEAAE	PPRDNQGF	CFVGLGEP	GLLLTKVYS	OOOPFVGY

```

RESULT 25
US-09-232-200-19
; Sequence 19, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MB
; CURRENT APPLICATION NUMBER: US/09232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-200-19

Query Match          24.3%; Score 54; DB 3; Length 199;
Best Local Similarity 28.6%; Fred.No. 50;
Matches 16; Conservative 5; Mismatches 7; Indels 28; Gaps 3;

```

Qy	4	NGAC-----SPPEV-----PPCRSRDCRCVPGL-----FVGf 31
		:     :     :
Dd	22	DGACLLRLMSPLVELVOFDMEAAFPVRDNOGCGTLPVGGCEPGHLLTKVVSOOOPVGY 77
		:     :     :

Search completed: March 28, 2005, 09:02:16

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:39:59 ; Search time 92 Seconds  
(without alignments)  
155.545 Million cell updates/sec

Title: US-09-674-496d-8

Perfect score: 222

Sequence: 1 ADNGACSPFEPVPCRSRDCRCVPIGLFVGFCIHPTG 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	100.0	37	3	AY55992 Insectici
2	155	69.8	37	3	AY55991 Insectici
3	154	69.4	37	3	AY55990 Insectici
4	76	34.2	18	4	AB85936 PALB seed
5	76	34.2	18	8	ADO21580 Pea album
6	67	30.2	158	4	AAU17088
7	67	30.2	158	7	AD93796 Novel sig
8	65	29.3	1250	4	ABG12917 Human nov
9	63	28.4	1216	4	ABG09754 Novel hum
10	63	28.4	2901	4	ABG09763 Novel hum
11	63	28.4	3075	2	AAW50892 Human lam
12	62.5	28.2	337	7	ADFA4673 Human NOV
13	62.5	28.2	337	8	ADO50858 Human NOV
14	62.5	28.2	343	7	ADFA4661 Human NOV
15	62.5	28.2	343	8	ADO50846 Human NOV
16	62.5	28.2	365	7	ADFA4659 Human NOV
17	62.5	28.2	365	7	ADFA4657 Human NOV
18	62.5	28.2	365	8	ADO50844 Human NOV
19	62.5	28.2	365	8	ADO50842 Human NOV
20	62.5	28.2	373	7	ADFA4663 Human NOV
21	62.5	28.2	373	8	ADO50848 Human NOV
22	62.5	28.2	375	7	ADFA4665 Human NOV
23	62.5	28.2	375	8	ADO50850 Human NOV
24	62.5	28.2	377	3	ADC78324 Human PRO
25	62.5	28.2	377	7	ADFA4671 Human NOV

26	62.5	28.2	377	8	ADO50856	Ado50856	Human	NOV
27	62.5	28.2	379	2	AY080065	Aay080065	Human	EGF
28	62.5	28.2	379	2	AA113345	Aay113345	Amino aci	
29	62.5	28.2	379	3	AY706669	Aay706669	Human	PRO
30	62.5	28.2	379	3	AA243397	Aab243397	Human	PRO
31	62.5	28.2	379	3	AY44822	Aay44822	Human	mol
32	62.5	28.2	379	4	AA80213	Aab80213	Human	PRO
33	62.5	28.2	379	4	AA31185	Aab31185	Amino aci	
34	62.5	28.2	379	4	AAU00822	Aau00822	Human	Imm
35	62.5	28.2	379	4	AAU12325	Aau12325	Human	Imm
36	62.5	28.2	379	4	AA853076	Aab53076	Human	ang
37	62.5	28.2	379	6	ABU71591	Abu71591	Human	PRO
38	62.5	28.2	379	6	ABO17769	Abu17769	Novel	hum
39	62.5	28.2	379	6	ABU71446	Abu71446	Human	PRO
40	62.5	28.2	379	6	ABO25156	Abu25156	Novel	hum
41	62.5	28.2	379	6	ABU81023	Abu81023	Human	PRO
42	62.5	28.2	379	6	ABU71892	Abu71892	Human	sec
43	62.5	28.2	379	6	ABO01775	Abu01775	Novel	hum
44	62.5	28.2	379	6	ABU66723	Abu66723	Human	PRO
45	62.5	28.2	379	6	ABU55917	Abu55917	Human	Wnt
46	62.5	28.2	379	6	ABU54348	Abu54348	Human	sec
47	62.5	28.2	379	6	ABU67274	Abu67274	Novel	hum
48	62.5	28.2	379	6	ABO47363	Abu47363	Human	sec
49	62.5	28.2	379	6	AAE34071	Aae34071	WIF-1	pro
50	62.5	28.2	379	6	ABU59804	Abu59804	Novel	sec
51	62.5	28.2	379	6	ABO24994	Abu24994	Human	sec
52	62.5	28.2	379	6	ABU64500	Abu64500	Human	sec
53	62.5	28.2	379	6	ABU72042	Abu72042	Novel	hum
54	62.5	28.2	379	6	ABU67346	Abu67346	Human	sec
55	62.5	28.2	379	6	ABU67143	Abu67143	Novel	hum
56	62.5	28.2	379	6	ABO14866	Abu14866	Human	sec
57	62.5	28.2	379	6	ABU66999	Abu66999	Human	sec
58	62.5	28.2	379	6	ABU69623	Abu69623	Novel	hum
59	62.5	28.2	379	6	ABU79785	Abu79785	Human	sec
60	62.5	28.2	379	6	ABO14805	Abu14805	Human	sec
61	62.5	28.2	379	6	ADA45827	Ada45827	Novel	hum
62	62.5	28.2	379	6	ADA76258	Ada76258	Human	PRO
63	62.5	28.2	379	6	ADB29209	Adb29209	Human	sec
64	62.5	28.2	379	6	ADA18908	Ada18908	Human	PRO
65	62.5	28.2	379	6	ADA61531	Ada61531	Homo sapi	
66	62.5	28.2	379	6	ADB19316	Adb19316	Novel	hum
67	62.5	28.2	379	6	ADB27857	Adb27857	Human	PRO
68	62.5	28.2	379	6	ADA86336	Ada86336	Novel	hum
69	62.5	28.2	379	6	ADB15900	Adb15900	Human	PRO
70	62.5	28.2	379	6	ADA47686	Ada47686	Human	PRO
71	62.5	28.2	379	6	ADA18065	Ada18065	Human	sec
72	62.5	28.2	379	6	ABO32757	Abu32757	Human	PRO
73	62.5	28.2	379	6	ADA67481	Ada67481	Human	PRO
74	62.5	28.2	379	6	ADB30488	Adb30488	Human	PRO
75	62.5	28.2	379	6	ADA85784	Ada85784	Novel	hum
76	62.5	28.2	379	6	ADA96996	Ada96996	Human	PRO
77	62.5	28.2	379	6	ADA79300	Ada79300	Human	PRO
78	62.5	28.2	379	6	ADA87439	Ada87439	Novel	hum
79	62.5	28.2	379	6	ADB16641	Adb16641	Human	PRO
80	62.5	28.2	379	6	ABO34817	Abu34817	Human	PRO
81	62.5	28.2	379	6	ADA16040	Ada16040	Human	sec
82	62.5	28.2	379	6	ADA91733	Ada91733	Novel	hum
83	62.5	28.2	379	6	ADB14796	Adb14796	Human	PRO
84	62.5	28.2	379	6	ADA71194	Ada71194	Human	sec
85	62.5	28.2	379	6	ADB18757	Adb18757	Novel	hum
86	62.5	28.2	379	6	ADA93972	Ada93972	Human	PRO
87	62.5	28.2	379	6	ADB19868	Adb19868	Novel	hum
88	62.5	28.2	379	6	ADB13180	Adb13180	Human	PRO
89	62.5	28.2	379	6	ABO43302	Abu43302	Novel	hum
90	62.5	28.2	379	6	ADA74434	Ada74434	Human	PRO
91	62.5	28.2	379	6	ADA42185	Ada42185	Human	sec
92	62.5	28.2	379	6	ADB24667	Adb24667	Human	PRO
93	62.5	28.2	379	6	ADA82191	Ada82191	Human	PRO
94	62.5	28.2	379	6	ADA75154	Ada75154	Human	PRO
95	62.5	28.2	379	6	ADA85232	Ada85232	Novel	hum
96	62.5	28.2	379	6	ADA84680	Ada84680	Novel	hum
97	62.5	28.2	379	6	ABO17495	Abu17495	Human	PRO
98	62.5	28.2	379	6	ADB29936	Adb29936	Human	PRO

99 62.5 28.2 379 6 ADA80464 Human PRO  
100 62.5 28.2 379 6 ADA75706 Human PRO

## ALIGNMENTS

RESULT 1  
AAV55992  
ID AAV55992 standard; peptide; 37 AA.

AC AAY55992;  
XX  
XX  
DT 15-MAR-2000 (first entry)  
XX  
DE Insecticidal peptide leguminsuline form soybean plants.  
XX  
XX  
KW Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;  
KW pest; Sitophilus oryzae; Ephestia kuehniella; Acyrthosiphon pisum;  
KW genetically modified organism.  
XX  
XX Glycine max.  
XX OS  
XX WO9958695-A1.  
XX PN  
XX XX  
PD 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-FR001085.  
XX PF  
XX XX  
PR 11-MAY-1998; 98FR-00005877.  
XX PR  
XX (NASC-) INST NAT SCI APPLIQUES LYON.  
PA (INRG) INST NAT RECH AGRONOMIQUE.  
XX  
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;  
XX WPI; 2000-062304/05.  
XX  
XX Use of polypeptide as insecticide, especially for controlling cereal  
PT grain pests.  
XX  
XX Example 2; Fig 7; 38pp; French.

This sequence represents the Cys-rich peptide sequence of legume plant  
derived insecticidal peptide leguminsuline corresponding to that of an  
entomotoxic pea protein. The invention relates to a novel insecticidal  
peptide PT (AAV55992) isolated from pea plants which has homology to the  
PALB peptide (AAV55991) and to the leguminsuline from soybeans. The  
insecticidal peptides preferably have the amino acid sequence:  
X1CYsX2CYsX3CYsX4CYsX5CYsX6CYsX7, where X1 = 2-10 amino acids; X2 = 2-5  
amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino  
acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal  
peptides can be used to protect cereal products or plants from attack by  
cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or  
Acyrthosiphon pisum, either directly or by genetically modifying plants  
(especially cereal plants) to express the peptide in their tissues or  
organs

SQ Sequence 37 AA;

Query Match 100.0%; Score 222; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2,2e-18;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADCNGACSPFVPPCSDRCRCVPIGLFVGFCIHPTG 37  
|||||  
DB 1 ADCNGACSPFVPPCSDRCRCVPIGLFVGFCIHPTG 37  
|||||

RESULT 2  
AAV55991  
ID AAV55991 standard; peptide; 37 AA.  
XX

AC AAY55991;  
XX  
XX  
DT 15-MAR-2000 (first entry)  
XX  
DE Insecticidal peptide PALB from pea plants.  
XX  
XX  
KW Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;  
KW pest; Sitophilus oryzae; Ephestia kuehniella; Acyrthosiphon pisum;  
KW genetically modified organism.  
XX  
XX Pisum sativum.  
XX OS  
XX WO9958695-A1.  
XX PN  
XX XX  
PD 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-FR001085.  
XX PF  
XX XX  
PR 11-MAY-1998; 98FR-00005877.  
XX PR  
XX (NASC-) INST NAT SCI APPLIQUES LYON.  
PA (INRG) INST NAT RECH AGRONOMIQUE.  
XX  
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;  
XX WPI; 2000-062304/05.  
XX  
XX Use of polypeptide as insecticide, especially for controlling cereal  
PT grain pests.  
XX  
XX Example 2; Fig 7; 38pp; French.

This sequence represents the Cys-rich peptide sequence of legume plant  
derived insecticidal peptide PALB corresponding to that of an entomotoxic  
pea protein. The invention relates to a novel insecticidal peptide PT  
(AAV55992) isolated from pea plants which has homology to the PALB  
peptide and to the leguminsuline from soybeans (AAV55991). The insecticidal  
peptides preferably have the amino acid sequence:  
X1CYsX2CYsX3CYsX4CYsX5CYsX6CYsX7, where X1 = 2-10 amino acids; X2 = 2-5  
amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino  
acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal  
peptides can be used to protect cereal products or plants from attack by  
cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or  
Acyrthosiphon pisum, either directly or by genetically modifying plants  
(especially cereal plants) to express the peptide in their tissues or  
organs

SQ Sequence 37 AA;

Query Match 69.8%; Score 155; DB 3; Length 37;  
Best Local Similarity 62.2%; Pred. No. 1.1e-10;  
Matches 23; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ADCNGACSPFVPPCSDRCRCVPIGLFVGFCIHPTG 37  
|||||  
DB 1 ASCNGVCSFPEMPPCGTSACRCIPVGLVVGVCYCRNPSG 37  
|||||

RESULT 3  
AAV55990  
ID AAV55990 standard; peptide; 37 AA.  
XX  
XX AAY55990;  
AC

XX  
XX  
DT 15-MAR-2000 (first entry)  
XX  
DE Insecticidal peptide PT from pea plants.  
XX

XX Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain;  
KW pest; Sitophilus oryzae; Ephestia kuehniella; Acyrthosiphon pisum;  
KW genetically modified organism.  
XX  
XX Pisum sativum.  
OS



```

XX W09958695-A1.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-FR001085.
PP
XX
XX 11-MAY-1998; 98FR-00005877.
PR
XX
XX (NASC-) INST NAT SCI APPLIQUES LYON.
PA
XX (INRG) INST NAT RECH AGRONOMIQUE.
PA
XX
XX Delobel B, Grenier A, Gueguen J, Ferrasson E, Mbailao M;
PI
XX
XX WPI; 2000-062304/05.
DR
XX
XX Use of polypeptide as insecticide, especially for controlling cereal
PT
XX grain pests.
PT
XX
XX Example 2; Fig 7; 38pp; French.
PS
XX
XX This sequence represents the Cys-rich peptide sequence of legume plant
CC derived insecticidal peptide PT corresponding to that of an entomotoxic
CC pea protein. The peptide has homology to the known insecticidal peptides
CC Palb (AAV55991) from peas or leguminosae (AAV55992) from soybeans. The
CC insecticidal peptides preferably have the amino acid sequence:
CC X1CYsX2CYsX3CYsX4CYsX5CYsX6CYsX7 where X1 = 2-10 amino acids; X2 = 2-5
CC amino acids; X3 = 4-10 amino acids; X4 = 3-10 amino acids; X5 = 2-4 amino
CC acids; X6 = 7-15 amino acids; and X7 = 2-10 amino acids. The insecticidal
CC peptide can be used to protect cereal products or plants from attack by
CC cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniella or
CC Acyrthosiphon pisum, either directly or by genetically modifying plants
CC (especially cereal plants) to express the peptide in their tissues or
CC organs
CC
XX
XX Sequence 37 AA;
SQ
Query Match 69.4%; Score 154; DB 3; Length 37;
Best Local Similarity 59.5%; Pred. No. 1.5e-10;
Matches 22; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 ADCNGACSPPEVPPCRSDRCRCVPIGLFVGFCIHPTG 37
DB 1 ASCNGVCSPEMPPCGTSACRCIPVGLVIGYCRNPSG 37
RESULT 4
AAB85936
ID AAB85936 standard; peptide; 18 AA.
XX
XX AAB85936;
AC
XX
XX 30-NOV-2001 (first entry)
DT
XX
XX Palb seed storage protein fragment.
DE
XX
XX Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
KW 2A11; PA1B.
XX
XX Unidentified.
OS
XX
XX US6281410-B1.
PN
XX
XX 28-AUG-2001.
PD
XX
XX 15-JAN-1999; 99US-00232861.
PF
XX
XX 31-JUL-1986; 86US-00891529.
PR
XX 26-MAY-1987; 87US-00054369.
PR 28-JUL-1987; 87US-00078538.
PR 25-JAN-1988; 88US-00147781.
PR 15-MAR-1988; 88US-00168190.
PR 29-APR-1988; 88US-00188361.
PR
XX
XX 02-NOV-1988; 88US-00267685.
PR 21-MAY-1990; 90US-00526123.
PR 09-JUL-1990; 90US-00550804.
PR 10-AUG-1993; 93US-00105852.
PR 07-JUN-1995; 95US-00484941.
PR 07-MAR-1997; 97US-00812665.
XX
XX (CALJ) CALGENE LLC.
PA
XX
XX Knauf VC, Kridl JC;
XX
XX WPI; 2001-564354/63.
DR
XX
XX Obtaining a plant that produces a seed with a modified phenotype or
PT altering a seed phenotype, comprises transforming a plant cell with a DNA
PT construct consisting of operably linked components in the direction of
PT transcription.
XX
XX Example 9; Fig 6; 68pp; English.
PS
XX
XX The invention provides a method for obtaining a plant which produces at
CC least one seed having a modified phenotype. The method involves
CC transforming a host plant cell with a DNA construct which consists of
CC operably linked components in the direction of transcription, a promoter
CC region from a Brassica plant gene, a DNA sequence of interest other than
CC the native coding sequence, and a transcription termination region. The
CC method is useful for obtaining plants having modified phenotype or for
CC altering the phenotype of a plant seed or tissue. The DNA constructs are
CC used in manipulating plant cells to provide for regulated transcription,
CC such as light inducible transcription, in a plant tissue or plant part of
CC interest at particular stages of plant growth or in response to external
CC control. These constructs are also used for modulation of expression of
CC endogenous products as well as production of exogenous products in the
CC seed. Sequences AAB85936-39 represent fragments of storage proteins used
CC in comparison studies with the storage protein 2A11
XX
XX Sequence 18 AA;
SQ
Query Match 34.2%; Score 76; DB 4; Length 18;
Best Local Similarity 64.7%; Pred. No. 0.073;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 7 CSPFEVPPCRSDRCRCV 23
DB 2 CSPFDIPPGSLCRCI 18
RESULT 5
ADO21580
ID ADO21580 standard; peptide; 18 AA.
XX
XX ADO21580;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Pea albumin 1b reactive site.
DE
XX
XX Pea; fruit specific promoter; plant; transgenic; protein storage;
KW improved nutrient source; enhanced response to light;
KW dehydration resistance; herbicide resistance; pest resistance; 2A11 gene;
KW protease inhibitor.
XX
XX Pisum sativum.
OS
XX
XX US2004055038-A1.
PN
XX
XX 18-MAR-2004.
PD
XX
XX 12-FEB-2001; 2001US-00782130.
PF
XX
XX 17-JAN-1985; 85US-00692605.
PR 31-JUL-1986; 86US-00891529.
PR 26-MAY-1987; 87US-00054369.
PR

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PR 28-JUL-1987; 87US-00078538.  
 PR 25-JAN-1988; 88US-00147781.  
 PR 15-MAR-1988; 88US-00168190.  
 PR 29-APR-1988; 88US-00188361.  
 PR 02-NOV-1988; 88US-00367685.  
 PR 21-MAY-1990; 90US-00262123.  
 PR 09-JUL-1990; 90US-00508084.  
 PR 14-SEP-1990; 90US-00592241.  
 PR 08-AUG-1991; 91US-00742834.  
 PR 10-AUG-1993; 93US-00105852.  
 PR 07-JUN-1995; 95US-00484941.  
 PR 07-MAR-1997; 97US-00812665.  
 PR 15-JAN-1999; 99US-00232861.  
 XX  
 PA (KNAU/) KNAUF V C.  
 PA (KRIDL/) KRIDL J C.  
 XX  
 XX Knauf VC, Kridl JC;  
 PI  
 XX WPI; 2004-247819/23.  
 DR  
 XX  
 XX  
 PT New DNA construct comprising a promoter region, a DNA sequence of  
 PT interest and a transcription termination region, useful for producing  
 PT transgenic plants.  
 XX  
 XX  
 FS Example 9; Fig 6; 68pp; English.  
 CC  
 CC The invention relates to a DNA construct comprising, as operably linked  
 CC components in the direction of transcription, a promoter region  
 CC obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier  
 CC protein (ACP) gene, a DNA sequence of interest other than the native  
 CC coding sequence of the gene and a transcription termination region, where  
 CC the components are functional in a plant cell and where the DNA construct  
 CC is flanked by T-DNA. Also included are a plant cell having an altered  
 CC phenotype as a result of expression of a DNA construct, a plant  
 CC comprising cells comprising a DNA construct, a seed obtained from the  
 CC plant, obtaining a plant having a modified phenotype or modifying the  
 CC genotype of a plant to impart a desired characteristic to seed as  
 CC distinct from other plant tissue, altering the phenotype of plant seed  
 CC tissue or modifying transcription in seed tissue as distinct from other  
 CC plant tissue and selectively expressing a heterologous DNA sequence of  
 CC interest in seed tissue as distinct from other plant tissue. The DNA  
 CC construct is useful in modifying or altering the genotype or phenotype of  
 CC a plant to impart a desired characteristic. The construct is also useful  
 CC in regulating genetic modification of plant or regulating tissue and/or  
 CC developmental specific transcription and expression in plants. The plants  
 CC produced have increased capability of protein storage, improved nutrient  
 CC source, enhanced response to light and dehydration resistance and  
 CC resistant to herbicide and pests. The seed specific promoters are from  
 CC the Napin, ACP and EA9 genes and the fruit specific promoter is from the  
 CC tomato 2A11 gene. The present sequence is a reactive site from a protein  
 CC similar to the tomato 2A11 protein (thought to be a protease inhibitor).  
 XX  
 SQ Sequence 18 AA;  
 Query Match 34.2%; Score 76; DB 8; Length 18;  
 Best Local Similarity 64.7%; Pred. No. 0.073;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 CSPFEVPPCRSDRCV 23  
 Db 2 CSPFDIPPGSLPCRCI 18  
 ||||:|||||  
 RESULT 6  
 AAU17088  
 ID AAU17088 standard; protein; 158 AA.  
 XX  
 AC AAU17088;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Novel signal transduction pathway protein, Seq ID 653.

XX  
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;  
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;  
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;  
 KW organ transplant rejection; infection; hepatitis C; blood disorder;  
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;  
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;  
 KW reproductive system; gastrointestinal; liver disorder; AIDS;  
 KW acquired immune deficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200154733-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001312.  
 PF  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226868P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234233P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234977P.  
PR 25-SEP-2000; 2000US-0234984P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-465460/50.  
XX N-PSDB; AAS27005.  
XX  
XX Novel polypeptides useful for diagnosing, treating, preventing and/or  
XX prognosing disorders related to the proteins, including cancers, immune  
XX disorders and neuronal disorders.  
XX  
XX Claim 1; SEQ ID NO 653; 880pp; English.  
XX  
XX The invention relates to novel isolated polypeptides (I), and  
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
XX diagnosing, preventing and treating diseases including immune system  
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
XX transplant rejections and graft versus host disease, infectious diseases  
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
XX other blood-related disorders (sickle cell anaemia), myeloproliferative  
XX disorders, primary haematopoietic disorders, hyperproliferative disorders  
XX (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.  
XX Alzheimer's disease, Parkinson's disease), chromosomal abnormalities  
XX (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.  
XX glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),  
XX respiratory disorders, dermatological disorders, in wound healing,  
XX epithelial cell proliferation, endocrine disorders (e.g. Addison's  
XX disease), reproductive system disorders, gastrointestinal disorder  
XX (inflammatory disorders), liver disorders (cirrhosis), as stimulators of  
XX B-cell responsiveness to pathogens, activators of T-cells, to induce  
XX higher affinity antibodies, and as a means to induce tumour proliferation  
XX in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU1059-  
XX AAU17683 represent novel signal transduction pathway protein, amino acid  
XX sequences of the invention  
XX  
Query Match 30.2%; Score 67; DB 4; Length 158;  
Best Local Similarity 32.6%; Pred. No. 5.4;  
Matches 14; Conservative 5; Mismatches 14; Indels 10; Gaps 1;  
Qy 5 GACSPFEVPCRSRDCRCVPIGLFVGFC-----IHPTG 37  
Db 96 GGQPSQPPPARASQCQPSLSQLFLGFCSQLVGPPTCALHPRG 138  
RESULT 7  
ADB93796  
ID ADB93796 standard; protein; 158 AA.  
XX  
XX ADB93796;  
XX  
XX 04-DEC-2003 (first entry)  
XX Human novel protein #30.  
XX  
XX human; autoimmune disease; Parkinson's disease; silicosis;  
XX gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;  
XX immunosuppressive agent; adjuvant; enhance immune response;  
XX higher affinity antibody induction;  
XX increased serum immunoglobulin concentration.  
XX

OS Homo sapiens.  
XX US2002168711-A1.  
XX 14-NOV-2002.  
XX 17-JAN-2001; 2001US-00764868.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 28-JUN-2000; 2000US-0211488P.  
XX 07-JUL-2000; 2000US-0211664P.  
XX 07-JUL-2000; 2000US-0216680P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225267P.  
XX 14-AUG-2000; 2000US-0225268P.  
XX 14-AUG-2000; 2000US-0225270P.  
XX 14-AUG-2000; 2000US-0225447P.  
XX 14-AUG-2000; 2000US-0225757P.  
XX 22-AUG-2000; 2000US-0225758P.  
XX 30-AUG-2000; 2000US-0226868P.  
XX 01-SEP-2000; 2000US-0228924P.  
XX 01-SEP-2000; 2000US-0229287P.  
XX 01-SEP-2000; 2000US-0229343P.  
XX 01-SEP-2000; 2000US-0229344P.  
XX 01-SEP-2000; 2000US-0229345P.  
XX 05-SEP-2000; 2000US-0229509P.  
XX 05-SEP-2000; 2000US-0229513P.  
XX 08-SEP-2000; 2000US-0231413P.  
XX 21-SEP-2000; 2000US-0234223P.  
XX 21-SEP-2000; 2000US-0234274P.  
XX 25-SEP-2000; 2000US-0234997P.  
XX 27-SEP-2000; 2000US-0235834P.  
XX 29-SEP-2000; 2000US-0236327P.  
XX 29-SEP-2000; 2000US-0236367P.  
XX 29-SEP-2000; 2000US-0236368P.  
XX 29-SEP-2000; 2000US-0236369P.  
XX 29-SEP-2000; 2000US-0236370P.  
XX 02-OCT-2000; 2000US-0236802P.  
XX 02-OCT-2000; 2000US-0237037P.  
XX 02-OCT-2000; 2000US-0237038P.  
XX 02-OCT-2000; 2000US-0237039P.  
XX 02-OCT-2000; 2000US-0237040P.  
XX 13-OCT-2000; 2000US-0239355P.  
XX 20-OCT-2000; 2000US-0240960P.  
XX 20-OCT-2000; 2000US-0241785P.  
XX 20-OCT-2000; 2000US-0241809P.  
XX 01-NOV-2000; 2000US-0244617P.  
XX 17-NOV-2000; 2000US-0249299P.  
XX 08-DEC-2000; 2000US-0251856P.  
XX 08-DEC-2000; 2000US-0251868P.  
XX 08-DEC-2000; 2000US-0251869P.  
XX (ROSE/) ROSEN C A.  
XX (RUBE/) RUBEN S M.  
XX (BARA/) BARASH S C.  
XX Rosen CA, Ruben SM, Barash SC;  
XX WPI; 2003-719985/68.  
XX N-PSDB; ADB93173.  
XX New isolated polypeptide useful for diagnosing and treating  
XX immunosuppressive conditions such as autoimmune disease and Parkinson's  
XX disease.  
XX Claim 11; SEQ ID NO 653; 345pp; English.  
XX

XX The invention relates to an isolated polypeptide. The polypeptide is  
XX useful for diagnosing a pathological condition or a susceptibility to a  
XX pathological condition in a subject, by determining the presence or  
XX amount of expression of the polypeptide in a biological sample and  
XX diagnosing a pathological condition or a susceptibility to a pathological  
XX condition based on the presence or amount of expression of the  
XX polypeptide. The polypeptide is also useful for identifying a binding  
XX partner to the polypeptide, which involves contacting the polypeptide  
XX with a binding partner and determining whether the binding partner  
XX effects an activity of the polypeptide. The polypeptide or the nucleic  
XX acid encoding the polypeptide is useful for preventing, treating, or  
XX ameliorating a medical condition, which involves administering the  
XX polypeptide or the nucleic acid to a mammalian subject. The nucleic acid  
XX is useful for diagnosing a pathological condition or a susceptibility to  
XX a pathological condition in a subject, which involves determining the  
XX presence or absence of a mutation in the nucleic acid, and diagnosing a  
XX pathological condition or susceptibility to a pathological condition  
XX based on the presence or absence of the mutation. The polypeptide, the  
XX nucleic acid and an antibody to the polypeptide are useful for treating  
XX autoimmune disease, Parkinson's disease, silicosis, gastrointestinal  
XX disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,  
XX as adjuvants to enhance immune responses, and as agents to induce higher  
XX affinity antibodies and increase serum immunoglobulin concentrations. The  
XX present sequence represents the amino acid sequence of a novel human  
XX protein. Note: The sequence data for this patent did not form part of the  
XX printed specification but was obtained in electronic format direct from  
XX USPTO at seqdata.uspto.gov/sequence.html?docID=20020168711.  
XX

SQ Sequence 158 AA;  
Query Match 30.2%; Score 67; DB 7; Length 158;  
Best Local Similarity 32.6%; Pred. No. 5.4;  
Matches 14; Conservative 5; Mismatches 14; Indels 10; Gaps 1;  
OY 5 GACSPFVPPCRSRDCRCPVIGLFGVFC-----IHPTG 37  
Db 96 GGQPSQPPPARASQCPQPSLQLFLGFCSQLVGPPTCALHPRG 138  
RESULT 8  
ABGI2917  
ID ABGI2917 standard; protein; 250 AA.  
XX AC ABGI2917;  
XX DT 13-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #12908.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX DR N-PSDB; AAS77104.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in



XX	WPI; 1998-240534/21.
XX	
XX	Use of laminin and fragments - for developing products for use in the
PT	diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
PT	CUD.
XX	
XX	Claim 15; Page 80-85; 132pp; English.
XX	
CC	This is the amino acid sequence of the human laminin A chain. The primary
CC	object of the invention is to use laminin, laminin-derived protein
CC	fragments and/or laminin-derived polypeptides as potent inhibitors of
CC	amyloid formation, deposition, accumulation and/or persistence in
CC	Alzheimer's disease and other amyloidoses. The laminin products (see
CC	AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1
CC	or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular
CC	repeats of the laminin A1 chain and the beta-amyloid binding domain of
CC	the laminin A chain. A claimed method for treating an amyloid disease
CC	comprises administering a polypeptide having a conformational similarity
CC	to a fragment of a laminin protein. A method for diagnosing an amyloid
CC	disease involves determining levels of laminin in a sample. Production of
CC	laminin or its fourth globular repeat in vivo provides a method for in
CC	vivo inhibition of beta-amyloid amyloidoses. The products and methods can
CC	be used for the diagnosis, prognosis, monitoring and treatment of
CC	amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary
CC	cerebral haemorrhage with amyloidosis of the Dutch type (where the
CC	specific amyloid is the beta-amyloid protein), the amyloidosis associated
CC	with chronic inflammation, various forms of malignancy and Familial
CC	Mediterranean Fever (AA amyloid or inflammation-association amyloidosis),
CC	the amyloidosis associated with multiple myeloma and other B-cell
CC	abnormalities (AL amyloid), the amyloidosis associated with type II
CC	diabetes (amylin or islet amyloid), the amyloidosis associated with prion
CC	diseases including Creutzfeldt-Jacob disease, Gerstmann-Straussler
CC	syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis
CC	associated with long-term haemodialysis and carpal tunnel syndrome (beta
CC	2-microglobulin amyloid), the amyloidosis associated with senile cardiac
CC	amyloid and Familial Amyloidotic Polyneuropathy (pralbumin or
CC	transthyretin amyloid), and the amyloidosis associated with endocrine
CC	tumours such as medullary carcinoma of the thyroid (variant of
CC	procalcitonin)
XX	
SQ	Sequence 3075 AA;
	Query Match 28.4%; Score 63; DB 2; Length 3075;
	Best Local Similarity 46.2%; Pred. No. 2-2e+02;
	Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY	8 SPEVPPCKSRDCRCVPDGLGVGFCCI 33   :         :   :   :
Db	387 SPYEDEPC--RPCNCDFVGSLSVCVI 410
RESULT 12	
ADFA4673	ID ID ADFA4673 standard; protein; 337 AA.
XX	AC ADF44673;
XX	
DT	12-FEB-2004 (first entry)
DE	Human NOV1j protein SEQ ID NO:20.
XX	
KW	human; antidiabetic; anorectic; cardiatic; hypotensive;
KW	antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW	protozoacide; antihelmintic; nootropic; neuroprotective;
KW	antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;
KW	antiinflammatory; dermatological; antiasthmatic; antilipaemic; vulnerary;
KW	antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;
KW	infectious disease; anorexia; cancer; cardiovascular disease;
KW	hypertension; atherosclerosis; neurodegenerative disorder;
KW	Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW	osteoarthritis; haematopoietic disorder; inflammatory skin disorder;
KW	asthma; dyslipidaemia.

XX OS Homo sapiens.  
 XX PN WO2003066881-A2.  
 XX PD 14-AUG-2003.  
 XX PF 03-FEB-2003; 2003WO-US003403.  
 XX PR 08-FEB-2002; 2002US-0355099P.  
 XX PR 12-FEB-2002; 2002US-00074978.  
 XX PR 12-FEB-2002; 2002US-0356424P.  
 XX PR 19-FEB-2002; 2002US-0357928P.  
 XX PR 21-FEB-2002; 2002US-0358608P.  
 XX PR 27-FEB-2002; 2002US-0359860P.  
 XX PR 25-APR-2002; 2002US-0375579P.  
 XX PR 01-MAY-2002; 2002US-00138588.  
 XX PR 17-MAY-2002; 2002US-0381666P.  
 XX PR 07-JUN-2002; 2002US-0387002P.  
 XX PR 02-JUL-2002; 2002US-0393285P.  
 XX PR 07-AUG-2002; 2002US-0401825P.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;  
 PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;  
 PI Stone DJ, Taupier RJ;  
 XX WPI; 2003-748127/70.  
 XX N-PSDB; ADF44672.  
 XX New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 XX Claim 1; SEQ ID NO 20; 234pp; English.  
 XX The present invention describes an isolated polypeptide (I) comprising:  
 CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n  
 CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a  
 CC sequence that is at least 95% identical to (P), or having one or more  
 CC conservative amino acid substitutions in. (I) can be encoded by a nucleic  
 CC acid molecule (II), where the sequence is selected from the group  
 CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,  
 CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,  
 CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,  
 CC neurotropic, neuroprotective, antiparkinsonian, anticonvulsant,  
 CC osteopathic, antiarthritic, antiinflammatory, dermatological,  
 CC antiasthmatic, antilipemic, vulnerary and angiogenic activities, and  
 CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules  
 CC (II) and antibodies that immunospecifically bind (I), can be used in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease. They are useful for treating, preventing or diagnosing  
 CC diseases such as metabolic disorders, diabetes, obesity, infectious diseases  
 CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,  
 CC cardiovascular diseases (hypertension, atherosclerosis),  
 CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,  
 CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,  
 CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and  
 CC (II) may also be used as targets for the identification of small  
 CC molecules that modulate or inhibit e.g. neurogenesis, cell  
 CC differentiation, cell proliferation, haematopoiesis, wound healing and  
 CC angiogenesis, in gene therapy, in gene ration of antibodies that bind  
 CC immunospecifically to (I) for use in therapeutic or diagnostic methods.  
 CC (I) can also be used as hybridisation probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX SQ Sequence 337 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 337;  
 Best Local Similarity 33.9%; Pred. No. 35;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;  
 Qy 1 ADCNGAC-----SPFEVPPCRSRTC--RCVPIGLFV--GFCIHPTG 37  
 Db 152 AECPGGCRNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPG 207  
 RESULT 13  
 ADO50858  
 ID ADO50858 standard; protein; 337 AA.  
 XX AC ADO50858;  
 XX DT 15-JUL-2004 (first entry)  
 XX DE Human NOV1j protein.  
 XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;  
 KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;  
 KW infection; haemophilia; graft-versus-host disease; AIDS;  
 KW acquired immune deficiency syndrome; asthma; Crohn's disease;  
 KW multiple sclerosis; anorexia; cancer-associated cachexia;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW haematopoietic disorder; dyslipidaemia; wasting disorder;  
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;  
 KW gene therapy; vaccine; human.  
 XX OS Homo sapiens.  
 XX PN US2004029140-A1.  
 XX PD 12-FEB-2004.  
 XX PF 16-JUL-2003; 2003US-00357820.  
 XX PR 04-OCT-2000; 2000US-00679460.  
 XX PR 05-DEC-2000; 2000US-00730617.  
 XX PR 08-FEB-2002; 2002US-0355099P.  
 XX PR 12-FEB-2002; 2002US-00074978.  
 XX PR 21-FEB-2002; 2002US-0357928P.  
 XX PR 19-FEB-2002; 2002US-0358608P.  
 XX PR 27-FEB-2002; 2002US-0359860P.  
 XX PR 25-APR-2002; 2002US-0375579P.  
 XX PR 01-MAY-2002; 2002US-00138588.  
 XX PR 17-JUN-2002; 2002US-0381666P.  
 XX PR 07-JUL-2002; 2002US-0387002P.  
 XX PR 02-JUL-2002; 2002US-0393265P.  
 XX (ANDE/) ANDERSON D W.  
 XX (BURG/) BURGESS C E.  
 XX (CASM/) CASMAN S J.  
 XX (GORM/) GORMAN L.  
 XX (JIW/) JI W.  
 XX (KEKU/) KEKUDA R.  
 XX (LILL/) LI L.  
 XX (PADI/) PADIGARU M.  
 XX (PATT/) PATTURAJAN M.  
 XX (PEN/) PENNA C E A.  
 XX (SHEN/) SHENOY S G.  
 XX (SHIM/) SHIMKETS R A.  
 XX (STON/) STONE D J.  
 XX (TAUP/) TAUPIER R J.  
 XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;  
 PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;  
 PI Stone DJ, Taupier RJ;  
 XX WPI; 2004-179665/17.  
 XX N-PSDB; ADO50857.  
 XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,  
 PT atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and  
 PT in chromosome mapping, tissue typing or pharmacogenomics.

XX PS Claim 1; SEQ ID NO 20; 119pp; English.

XX CC The present invention relates to novel NOVX polypeptides and their

CC encoding polynucleotides. The invention is useful in diagnosing, treating

CC and preventing NOVX-associated disorders such as cardiomyopathy,

CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune

CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,

CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as

CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,

CC dyslipidaemia and other wasting disorders associated with chronic

CC diseases. The invention is also useful as hybridisation probes, in

CC chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. The invention is also useful in gene therapy and in the

CC preparation of vaccines. The present sequence is human NOVX protein.

XX SQ Sequence 337 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 337;

Best Local Similarity 33.9%; Pred. No. 35;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37

Db 152 AECFGGCRNGGFCNERRICPCDGFHGHCEKALCTPRCNGGLCVTPGFCICPPG 207

RESULT 14

ADF44661

ID ADF44661 standard; protein; 343 AA.

AC ADF44661;

XX DT 12-FEB-2004 (first entry)

XX DE Human NOV1d protein SEQ ID NO:8.

XX KW human; antidiabetic; anorectic; cardiant; hypotensive;

KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;

KW protozoacide; antihelminthic; nootropic; neuroprotective;

KW antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;

KW antiinflammatory; dermatological; antiasthmatic; antipneumonic; vulnary;

KW antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;

KW infectious disease; anorexia; cancer; cardiovascular disease;

KW hypertension; atherosclerosis; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;

KW osteoarthritis; haematopoietic disorder; inflammatory skin disorder;

KW asthma; dyslipidaemia.

XX OS Homo sapiens.

XX PN W02003066881-A2.

XX PD 14-AUG-2003.

XX PF 03-FEB-2003; 2003WO-US003403.

XX PR 08-FEB-2002; 2002US-0355099P.

PR 12-FEB-2002; 2002US-00074978.

PR 12-FEB-2002; 2002US-0356424P.

PR 13-FEB-2002; 2002US-0357928P.

PR 21-FEB-2002; 2002US-0358608P.

PR 27-FEB-2002; 2002US-0359860P.

PR 25-APR-2002; 2002US-0375579P.

PR 01-MAY-2002; 2002US-00138588.

PR 17-MAY-2002; 2002US-0381666P.

PR 07-JUN-2002; 2002US-0387002P.

PR 02-JUL-2002; 2002US-0393265P.

PR 07-AUG-2002; 2002US-0401825P.

XX PA (CURA-) CURAGEN CORP.

PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

PI Li L, Padigar M, Patturajan M, Pena CE, Shenoy SG, Shinkets RA;

PI Stone DJ, Taupier RJ;

XX WPI; 2003-748127/70.

DR N-PSDB; ADF44660.

XX PT New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX PS Claim 1; SEQ ID NO 8; 234pp; English.

XX CC The present invention describes an isolated polypeptide (I) comprising:

CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n

CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a

CC sequence that is at least 95% identical to (P), or having one or more

CC conservative amino acid substitutions in. (I) can be encoded by a nucleic

CC acid molecule (II), where the sequence is selected from the group

CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,

CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,

CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,

CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,

CC osteopathic, antiarthritic, antiinflammatory, dermatological,

CC antiasthmatic, antipneumonic, vulnary and antiangiogenic activities, and

CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules

CC (II) and antibodies that immunospecifically bind (I), can be used in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease. They are useful for treating, preventing or diagnosing

CC diseases such as metabolic disorders, diabetes, obesity, infectious diseases

CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,

CC cardiovascular diseases (hypertension, atherosclerosis),

CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,

CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,

CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and

CC (II) may also be used as targets for the identification of small

CC molecules that modulate or inhibit e.g. neurogenesis, cell

CC differentiation, cell proliferation, haematopoiesis, wound healing and

CC angiogenesis, in gene therapy, in gene ration of antibodies that bind

CC immunospecifically to (I) for use in therapeutic or diagnostic methods.

CC (I) can also be used as hybridisation probes, in chromosome mapping,

CC tissue typing, preventive medicine, and pharmacogenomics. The present

CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 343 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 343;

Best Local Similarity 33.9%; Pred. No. 36;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37

Db 155 AECFGGCRNGGFCNERRICPCDGFHGHCEKALCTPRCNGGLCVTPGFCICPPG 210

RESULT 15

ADO50846

ID ADO50846 standard; protein; 343 AA.

XX AC ADO50846;

XX DT 15-JUL-2004 (first entry)

XX DE Human NOV1d protein.

XX KW NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

KW infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;

KW multiple sclerosis; anorexia; cancer-associated cachexia;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW haematopoietic disorder; dyslipidaemia; wasting disorder;



KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;  
 KW gene therapy; vaccine; human.

OS Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

XX (BURG/) BURGESS C E.

XX (CASM/) CASMAN S J.

XX (GORM/) GORMAN L.

XX (JIW/) JI W.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (PADI/) PADIGARU M.

XX (PATT/) PATTURAJAN M.

XX (PENA/) PENNA C E A.

XX (SHIM/) SHIMOY S G.

XX (SHIM/) SHIMKETS R A.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

XX Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;

XX Stone DJ, Taupier RJ;

XX WPI; 2004-179665/17.

XX N-PSDB; ADO50845.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

XX atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and

XX in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; SEQ ID NO 8; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their

XX encoding polynucleotides. The invention is useful in diagnosing, treating

XX and preventing NOVX-associated disorders such as cardiomyopathy,

XX atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

XX infections, haemophilia, graft-versus-host disease, AIDS (acquired immune

XX deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,

XX anorexia, cancer-associated cachexia, neurodegenerative disorders such as

XX Alzheimer's disease, Parkinson's disease, haematopoietic disorders,

XX dyslipidaemias and other wasting disorders associated with chronic

XX diseases. The invention is also useful as hybridisation probes, in

XX chromosome mapping, tissue typing, preventive medicine and

XX pharmacogenomics. The invention is also useful in gene therapy and in the

XX preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 343 AA;

XX Query Match 28.2%; Score 62.5; DB 8; Length 343;

XX Best Local Similarity 33.9%; Pred. No. 36;

XX Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

XX 1 ACNCGAC-----SPFEVPPCRSDDC--RCVPIGLFV--GFCIHPTG 37

Db

RESULT 16

ADF44659

XX ADF44659 standard; protein; 365 AA.

XX ADF44659;

XX 12-FEB-2004 (first entry)

XX Human NOV1c protein SEQ ID NO:6.

XX human; antidiabetic; anorectic; cardiant; hypotensive;  
 KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;  
 KW protozoacide; antihelminthic; nootropic; neuroprotective;  
 KW antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;  
 KW antiinflammatory; dermatological; antiasthmatic; antilipemic; vulnary;  
 KW antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;  
 KW infectious disease; anorexia; cancer; cardiovascular disease;  
 KW hypertension; atherosclerosis; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;  
 KW osteoarthritis; haematopoietic disorder; inflammatory skin disorder;  
 KW asthma; dyslipidaemia.

XX Homo sapiens.

XX WO2003066881-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-US003403.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 12-FEB-2002; 2002US-0356424P.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX 07-AUG-2002; 2002US-0401825P.

XX (CURA-) CURAGEN CORP.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

XX Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;

XX Stone DJ, Taupier RJ;

XX WPI; 2003-748127/70.

XX N-PSDB; ADF44659.

XX New isolated NOVX polypeptides and polynucleotides, useful for

XX preventing, diagnosing or treating NOVX-associated disorders, e.g.

XX osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

XX asthma, or infections.

XX Claim 1; SEQ ID NO 6; 234pp; English.

XX The present invention describes an isolated polypeptide (I) comprising:

XX (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n

XX is an integer between 1 and 34); (b) a mature form of (a); or (c) a

XX sequence that is at least 95% identical to (P), or having one or more

XX conservative amino acid substitutions in. (I) can be encoded by a nucleic

XX acid molecule (II), where the sequence is selected from the group

XX consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,

XX anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,

XX virucide, antibacterial, fungicide, protozoacide, antihelminthic,

XX nootropic, neuroprotective, antiparkinsonian, anticonvulsant,

osteopathic, antiarthritic, antiinflammatory, dermatological, antiasthmatic, antilipemic, vulnery and antiangiogenic activities, and can be used in gene therapy. The polypeptides (I), nucleic acid molecules (II) and antibodies that immunospecifically bind (I), can be used in the manufacture of a medicament for treating a syndrome associated with a human disease. They are useful for treating, preventing or diagnosing diseases such metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders (Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders (osteoarthritis), haematopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and (II) may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in gene ration of antibodies that bind immunospecifically to (I) for use in therapeutic or diagnostic methods. (I) can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is used in the exemplification of the present invention.

XX Sequence 365 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 365;  
Best Local Similarity 33.9%; Pred. No. 38;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37  
DB 180 AECFGCGNGGFCNERRICECDGPHGHCALCTPRCMNGGCVTFGFCICPPG 235

RESULT 17  
ADF44657

ID ADF44657 standard; protein; 365 AA.

XX ADF44657;

DT 12-FEB-2004 (first entry)

DE Human NOV1b protein SEQ ID NO:4.

human; antidiabetic; anorectic; cardiant; hypotensive;  
antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;  
protozoacide; antihelminthic; nootropic; neuroprotective;  
antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;  
antiinflammatory; dermatological; antiasthmatic; antilipemic; vulnery;  
antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;  
infectious disease; anorexia; cancer; cardiovascular disease;  
hypertension; atherosclerosis; neurodegenerative disorder;  
Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;  
osteoarthritis; haematopoietic disorder; inflammatory skin disorder;  
asthma; dyslipidaemia.

OS Homo sapiens.

XX W02003066881-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-US003403.  
XX 08-FEB-2002; 2002US-0355099P.  
PR 12-FEB-2002; 2002US-00074978.  
PR 12-FEB-2002; 2002US-0356424P.  
PR 19-FEB-2002; 2002US-0357928P.  
PR 21-FEB-2002; 2002US-0358608P.  
PR 27-FEB-2002; 2002US-0359860P.  
PR 25-APR-2002; 2002US-0375799P.  
PR 01-MAY-2002; 2002US-00138588.  
PR 07-MAY-2002; 2002US-0381666P.  
PR 17-JUN-2002; 2002US-0387002P.  
PR 02-JUL-2002; 2002US-0393265P.

PR 07-AUG-2002; 2002US-0401825P.

XX (CURA-) CURAGEN CORP.

FA Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;  
PI Li L, Padigaru M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;  
PI Stone DJ, Taupier RJ;

XX WPI; 2003-748127/70.

DR N-PSDB; ADF44656.

XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
PT asthma, or infections.

PS Claim 1; SEQ ID NO 4; 234pp; English.

XX The present invention describes an isolated polypeptide (I) comprising:  
CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n  
CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a  
CC sequence that is at least 95% identical to (P), or having one or more  
CC conservative amino acid substitutions in. (I) can be encoded by a nucleic  
CC acid molecule (II), where the sequence is selected from the group  
CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,  
CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,  
CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,  
CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,  
CC osteopathic, antiarthritic, antiinflammatory, dermatological,  
CC antiasthmatic, antilipemic, vulnery and antiangiogenic activities, and  
CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules  
CC (II) and antibodies that immunospecifically bind (I), can be used in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease. They are useful for treating, preventing or diagnosing  
CC diseases such metabolic disorders, diabetes, obesity, infectious diseases  
CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,  
CC cardiovascular diseases (hypertension, atherosclerosis),  
CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,  
CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,  
CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and  
CC (II) may also be used as targets for the identification of small  
CC molecules that modulate or inhibit e.g. neurogenesis, cell  
CC differentiation, cell proliferation, haematopoiesis, wound healing and  
CC angiogenesis, in gene therapy, in gene ration of antibodies that bind  
CC immunospecifically to (I) for use in therapeutic or diagnostic methods.  
CC (I) can also be used as hybridisation probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. The present  
CC sequence is used in the exemplification of the present invention.

XX Sequence 365 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 365;  
Best Local Similarity 33.9%; Pred. No. 38;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37  
DB 180 AECFGCGNGGFCNERRICECDGPHGHCALCTPRCMNGGCVTFGFCICPPG 235

RESULT 18

ADO50844

ID ADO50844 standard; protein; 365 AA.

XX ADO50844;

DT 15-JUL-2004 (first entry)

XX Human NOV1c protein.

DE NOX; diagnosis; NOVX-associated disorder; cardiomyopathy;  
KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;  
KW infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;  
 KW multiple sclerosis; anorexia; cancer-associated cachexia;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW haematopoietic disorder; dyslipidaemia; wasting disorder;  
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;  
 KW gene therapy; vaccine; human.

XX Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

XX (BURG/) BURGESS C E.

XX (CASM/) CASMAN S J.

XX (GORM/) GORMAN L.

XX (JIWW/) JI W.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (PADI/) PADIGARU M.

XX (PATT/) PATTURAJAN M.

XX (PENA/) PENA C E A.

XX (SHEN/) SHENOY S G.

XX (SHIM/) SHIMKETS R A.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

XX Li L, Padigar M, Patturajan M, Pena CE, Shenoy SG, Shimkets RA;

XX Stone DJ, Taupier RJ;

XX WPI; 2004-179665/17.

XX N-PSDB; ADO50843.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

PT atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and  
 PT in chromosome mapping, tissue typing or pharmacogenomics.  
 XX Claim 1; SEQ ID NO 6; 119pp; English.  
 XX The present invention relates to novel NOVX polypeptides and their  
 CC encoding polynucleotides. The invention is useful in diagnosing, treating  
 CC and preventing NOVX-associated disorders such as cardiomyopathy, cancer  
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
 CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune  
 CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,  
 CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as  
 CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,  
 CC dyslipidaemias and other wasting disorders associated with chronic  
 CC diseases. The invention is also useful as hybridisation probes, in  
 CC chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. The invention is also useful in gene therapy and in the  
 CC preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 365 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 365;

Best Local Similarity 33.9%; Pred. No. 38;  
 Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;  
 Qy 1 A D C N G A C ----- S P F E V P P C R S R D C -- R C V P I G L F V -- G F C I H P T G 37  
 Db 180 A E C P G G C R N G G F C N E R R I C E C P D G F H P C E K A L C T P R C M N G G L C V T P G F C I C P P G 235

RESULT 19

ADO50842

ID ADO50842 standard; protein; 365 AA.

XX ADO50842;

XX 15-JUL-2004 (first entry)

XX Human NOV1b protein.

XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

KW infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;

KW multiple sclerosis; anorexia; cancer-associated cachexia;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW haematopoietic disorder; dyslipidaemia; wasting disorder;

KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;

KW gene therapy; vaccine; human.

XX Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381666P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.

XX (BURG/) BURGESS C E.

XX (CASM/) CASMAN S J.

XX (GORM/) GORMAN L.

XX (JIWW/) JI W.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (PADI/) PADIGARU M.

XX (PATT/) PATTURAJAN M.

XX (PENA/) PENA C E A.

XX (SHEN/) SHENOY S G.

XX (SHIM/) SHIMKETS R A.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

XX Li L, Padigar M, Patturajan M, Pena CE, Shenoy SG, Shimkets RA;

XX Stone DJ, Taupier RJ;

XX WPI; 2004-179665/17.

XX N-PSDB; ADO50841.

XX New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,

XX atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and

PT in chromosome mapping, tissue typing or pharmacogenomics.

PS Claim 1; SEQ ID NO 4; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their  
 CC encoding polynucleotides. The invention is useful in diagnosing, treating  
 CC and preventing NOVX-associated disorders such as cardiomyopathy,  
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
 CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune  
 CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,  
 CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as  
 CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,  
 CC dyslipidaemias and other wasting disorders associated with chronic  
 CC diseases. The invention is also useful as hybridisation probes, in  
 CC chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. The invention is also useful in gene therapy and in the  
 CC preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 365 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 365;

Best Local Similarity 33.9%; Pred. No. 38;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Oy 1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37  
 Db 180 AECPGGCRNGFCNERRICECPDGFHGHCEKALCTPRCNGGLCVTPGFCICPPG 235

RESULT 20

ADF4663

ID ADF4663 standard; protein; 373 AA.

XX ADF4663;

DT 12-FEB-2004 (first entry)

DE Human NOV1e protein SEQ ID NO:10.

XX human; antidiabetic; anorectic; cardiant; hypotensive;  
 KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;  
 KW protozoacide; antihelminthic; nootropic; neuroprotective;  
 KW antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;  
 KW antiinflammatory; dermatological; antiasthmatic; antilipaeamic;  
 KW antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;  
 KW infectious disease; anorexia; cancer; cardiovascular disease;  
 KW hypertension; atherosclerosis; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;  
 KW osteoarthritis; haematopoietic disorder; inflammatory skin disorder;  
 KW asthma; dyslipidaemia.

OS Homo sapiens.

XX WO2003066881-A2.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-US003403.

XX 08-FEB-2002; 2002US-0355099P.

PR 13-FEB-2002; 2002US-00074978.

PR 12-FEB-2002; 2002US-0356424P.

PR 19-FEB-2002; 2002US-0357928P.

PR 21-FEB-2002; 2002US-0358608P.

PR 27-FEB-2002; 2002US-0375579P.

PR 25-APR-2002; 2002US-00138588.

PR 01-MAY-2002; 2002US-0381666P.

PR 17-MAY-2002; 2002US-0387002P.

PR 07-JUN-2002; 2002US-0393265P.

PR 02-JUL-2002; 2002US-0393265P.

PR 07-AUG-2002; 2002US-0401825P.

XX (CURA-) CURAGEN CORP.

XX

PI Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;

PI Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;

PI Stone DJ, Taupier RJ;

XX

DR WPI; 2003-748127/70.

DR N-PSDB; ADF44662.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX

PS Claim 1; SEQ ID NO 10; 234pp; English.

XX

CC The present invention describes an isolated polypeptide (I) comprising:

CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n

CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a

CC sequence that is at least 95% identical to (P), or having one or more

CC conservative amino acid substitutions in. (I) can be encoded by a nucleic

CC acid molecule (II), where the sequence is selected from the group

CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,

CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,

CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,

CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,

CC osteopathic, antiarthritic, antilipaeamic, antiinflammatory, anticonvulsant,

CC antiasthmatic, antilipaeamic, vulnery and antiangiogenic activities, and

CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules

CC (II) and antibodies that immunospecifically bind (I), can be used in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease. They are useful for treating a syndrome associated with a

CC diseases such metabolic disorders, diabetes, obesity, infectious diseases

CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,

CC cardiovascular diseases (hypertension, atherosclerosis),

CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,

CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,

CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and

CC (II) may also be used as targets for the identification of small

CC molecules that modulate or inhibit e.g. neurogenesis, cell

CC differentiation, cell proliferation, haematopoiesis, wound healing and

CC angiogenesis, in gene therapy, in gene ration of antibodies that bind

CC immunospecifically to (I) for use in therapeutic or diagnostic methods.

CC (I) can also be used as hybridisation probes, in chromosome mapping,

CC tissue typing, preventive medicine, and pharmacogenomics. The present

CC sequence is used in the exemplification of the present invention.

XX

SQ Sequence 373 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 373;

Best Local Similarity 33.9%; Pred. No. 39;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Oy 1 ADCNGAC-----SPFEVPPCRSDC--RCVPIGLFV--GFCIHPTG 37

Db 185 AECPGGCRNGFCNERRICECPDGFHGHCEKALCTPRCNGGLCVTPGFCICPPG 240

RESULT 21

ADO50848

ID ADO50848 standard; protein; 373 AA.

XX ADO50848;

DT 15-JUL-2004 (first entry)

DE Human NOV1e protein.

XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;

KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;

KW infection; haemophilia; graft-versus-host disease; AIDS;

KW acquired immune deficiency syndrome; asthma; Crohn's disease;

KW multiple sclerosis; anorexia; cancer-associated cachexia;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;



CC nootropic, neuroprotective, antiparkinsonian, anticonvulsant,  
 CC osteopathic, antiarthritic, antiinflammatory, dermatological,  
 CC antiasthmatic, antipalemic, vulnerary and antiangiogenic activities, and  
 CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules  
 CC (II) and antibodies that immunospecifically bind (I), can be used in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease. They are useful for treating, preventing or diagnosing  
 CC diseases such metabolic disorders, diabetes, obesity, infectious diseases  
 CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,  
 CC cardiovascular diseases (hypertension, atherosclerosis),  
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,  
 CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,  
 CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and  
 CC (II) may also be used as targets for the identification of small  
 CC molecules that modulate or inhibit e.g. neurogenesis, cell  
 CC differentiation, cell proliferation, haematopoiesis, wound healing and  
 CC angiogenesis, in gene therapy, in gene ration of antibodies that bind  
 CC immunospecifically to (I) for use in therapeutic or diagnostic methods.  
 CC (I) can also be used as hybridisation probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 375 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 375;  
 Best Local Similarity 33.9%; Pred. No. 39;  
 Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPPEVPPCRSRDC--RCVPGLFLV--GFCIHPTG 37  
 Db 176 AECGGCRNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTFGFCICPPG 231

RESULT 23

AD050850

ID AD050850 standard; protein; 375 AA.

AC AD050850;

XX 15-JUL-2004 (first entry)

XX Human NOV1f protein.

XX NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;  
 KW atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes;  
 KW infection; haemophilia; graft-versus-host disease; AIDS;  
 KW acquired immune deficiency syndrome; asthma; Crohn's disease;  
 KW multiple sclerosis; anorexia; cancer-associated cachexia;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW haematopoietic disorder; dyslipidaemia; wasting disorder;  
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;  
 KW gene therapy; vaccine; human.

XX Homo sapiens.

XX US2004029140-A1.

XX 12-FEB-2004.

XX 16-JUL-2003; 2003US-00357820.

XX 04-OCT-2000; 2000US-00679460.

XX 05-DEC-2000; 2000US-00730617.

XX 08-FEB-2002; 2002US-0355099P.

XX 12-FEB-2002; 2002US-00074978.

XX 19-FEB-2002; 2002US-0357928P.

XX 21-FEB-2002; 2002US-0358608P.

XX 27-FEB-2002; 2002US-0359860P.

XX 25-APR-2002; 2002US-0375579P.

XX 01-MAY-2002; 2002US-00138588.

XX 17-MAY-2002; 2002US-0381566P.

XX 07-JUN-2002; 2002US-0387002P.

XX 02-JUL-2002; 2002US-0393265P.

XX (ANDE/) ANDERSON D W.  
 PA (BURG/) BURGESS C E.  
 PA (CASM/) CASMAN S J.  
 PA (GORM/) GORMAN L.  
 PA (JIWW/) JI W.  
 PA (KEKU/) KEKUDA R.  
 PA (LILL/) LI L.  
 PA (PADI/) PADIGARU M.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (SHEN/) SHENY S G.  
 PA (SHIM/) SHIMKETS R A.  
 PA (STON/) STONE D J.  
 PA (TAUP/) TAUFIER R J.

Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;  
 Li L, Padigar M, Patturajan M, Pena CEA, Shenoy SG, Shimketa RA;  
 Stone DJ, Taupier RJ;

WPI; 2004-179665/17.  
 N-PSDB; AD050849.

New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes,  
 PT atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and  
 PT in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; SEQ ID NO 12; 119pp; English.

XX The present invention relates to novel NOVX polypeptides and their  
 CC encoding polynucleotides. The invention is useful in diagnosing, treating  
 CC and preventing NOVX-associated disorders such as cardiomyopathy,  
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
 CC infections, haemophilia, graft-versus-host disease, AIDS (acquired immune  
 CC deficiency syndrome), asthma, Crohn's disease, multiple sclerosis,  
 CC anorexia, cancer-associated cachexia, neurodegenerative disorders such as  
 CC Alzheimer's disease, Parkinson's disease, haematopoietic disorders,  
 CC dyslipidaemias and other wasting disorders associated with chronic  
 CC diseases. The invention is also useful as hybridisation probes, in  
 CC chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. The invention is also useful in gene therapy and in the  
 CC preparation of vaccines. The present sequence is human NOVX protein.

XX Sequence 375 AA;

Query Match 28.2%; Score 62.5; DB 8; Length 375;  
 Best Local Similarity 33.9%; Pred. No. 39;

Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

QY 1 ADCNGAC-----SPPEVPPCRSRDC--RCVPGLFLV--GFCIHPTG 37

Db 176 AECGGCRNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTFGFCICPPG 231

RESULT 24

ADC78324

ID ADC78324 standard; protein; 377 AA.

XX ADC78324;

XX 01-JAN-2004 (first entry)

XX Human PRO217 protein.

XX antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;  
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;  
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;  
 KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;  
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;  
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;  
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;  
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;  
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;

KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;  
KW diabetes; stroke; gene therapy; transgenic; PRO; human.  
XX Homo sapiens.  
XX WO200015796-A2.  
XX 23-MAR-2000.  
XX 15-SEP-1999; 99WO-US021090.  
XX 16-SEP-1998; 98WO-US019330.  
XX (SETH ) GENENTECH INC.  
XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WT;  
PI Yuan J;  
XX WPI; 2000-271434/23.  
DR N-PSDB; ADC78323.  
XX Novel nucleic acids encoding secreted and transmembrane polypeptides with  
PT homology, e.g. to growth and cancer-associated antigens.  
XX Claim 12; SEQ ID NO 4; 355pp; English.  
XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.  
CC The polypeptides and polynucleotides of the invention may be useful as  
CC research tools and as therapeutics for treating enterocolitis, Zollinger-  
CC Ellison syndrome, gastrointestinal ulceration, peoriasis, cancer,  
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal  
CC scarring and wound healing, nerve repair, thrombosis, bone and/or  
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple  
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,  
CC infertility, premature aging, AIDS, diabetes complications and stroke.  
CC The molecules may also be utilised during gene therapy procedures and  
CC transgenic animal production. The current sequence is that of the human  
CC PRO protein of the invention.  
XX  
SQ Sequence 377 AA;  
Query Match 28.2%; Score 62.5; DB 3; Length 377;  
Best Local Similarity 33.9%; Pred. No. 39;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;  
QY 1 ADCNGAC-----SPFEVPPCKSRDC--RCVPIGLFLV--GFCIHPTG 37  
DB 179 AECFGCGNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTFGFCICPPG 234  
RESULT 25  
ID ADF44671  
XX ADF44671 standard; protein; 377 AA.  
XX ADF44671;  
XX 12-FEB-2004 (first entry)  
XX Human NOV1 protein SEQ ID NO:18.  
XX human; antidiabetic; anorectic; cardiant; hypotensive;  
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;  
KW protozoacide; antihelminthic; nontropic; neuroprotective;  
KW antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;  
KW antiinflammatory; dermatological; antiaesthetic; antilipemic; vulnery;  
KW antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity;  
KW infectious disease; anorexia; cancer; cardiovascular disease;  
KW hypertension; atherosclerosis; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;  
KW osteoarthritis; haematopoietic disorder; inflammatory skin disorder;  
KW asthma; dyslipidaemia.  
XX Homo sapiens.

XX WO2003066881-A2.  
XX 14-AUG-2003.  
XX 03-FEB-2003; 2003WO-US003403.  
XX 08-FEB-2002; 2002US-0355099P.  
PR 12-FEB-2002; 2002US-00074978.  
PR 12-FEB-2002; 2002US-0356424P.  
PR 19-FEB-2002; 2002US-0357928P.  
PR 21-FEB-2002; 2002US-0358608P.  
PR 27-FEB-2002; 2002US-0359850P.  
PR 25-APR-2002; 2002US-0375579P.  
PR 01-MAY-2002; 2002US-00138588.  
PR 17-MAY-2002; 2002US-0381666P.  
PR 07-JUN-2002; 2002US-0387002P.  
PR 02-JUL-2002; 2002US-0393265P.  
PR 07-AUG-2002; 2002US-0401825P.  
XX (CURA-) CURAGEN CORP.  
XX Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;  
PI Li L, Radigar M, Batturajan M, Pena CEA, Shenoy SG, Shimkets RA;  
PI Stone DJ, Taupier RJ;  
XX WPI; 2003-748127/70.  
DR N-PSDB; ADF44670.  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
PT asthma, or infections.  
XX Claim 1; SEQ ID NO 18; 234pp; English.  
XX The present invention describes an isolated polypeptide (I) comprising:  
CC (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n  
CC is an integer between 1 and 34); (b) a mature form of (a); or (c) a  
CC sequence that is at least 95% identical to (P), or having one or more  
CC conservative amino acid substitutions in. (I) can be encoded by a nucleic  
CC acid molecule (II), where the sequence is selected from the group  
CC consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic,  
CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,  
CC virucide, antibacterial, fungicide, protozoacide, antihelminthic,  
CC nontropic, neuroprotective, antiparkinsonian, anticonvulsant,  
CC osteopathic, antiarthritic, antiinflammatory, dermatological,  
CC antiasthmatic, antilipemic, vulnery and antiangiogenic activities, and  
CC can be used in gene therapy. The polypeptides (I), nucleic acid molecules  
CC (II) and antibodies that immunospecifically bind (I), can be used in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease. They are useful for treating, preventing or diagnosing  
CC diseases such as metabolic disorders, diabetes, obesity, infectious diseases  
CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,  
CC cardiovascular diseases (hypertension, atherosclerosis),  
CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,  
CC epilepsy, immune disorders (osteoarthritis), haematopoietic disorders,  
CC inflammatory skin disorders, asthma, and various dyslipidaemias. (I) and  
CC (II) may also be used as targets for the identification of small  
CC molecules that modulate or inhibit e.g. neurogenesis, cell  
CC differentiation, cell proliferation, haematopoiesis, wound healing and  
CC angiogenesis, in gene therapy, in gene ration of antibodies that bind  
CC immunospecifically to (I) for use in therapeutic or diagnostic methods.  
CC (I) can also be used as hybridisation probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 377 AA;

Query Match 28.2%; Score 62.5; DB 7; Length 377;  
Best Local Similarity 33.9%; Pred. No. 39;  
Matches 19; Conservative 2; Mismatches 16; Indels 19; Gaps 3;

Qy 1 ADCNGAC-----SPEFVPPCRSRTC--RCVPFGLFV--GFCIHFTG 37  
Db 176 AECPGGCRNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTFGFCICPPG 231

Search completed: March 28, 2005, 08:57:12  
Job time : 96 secs